

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number

TO: Louis V Wollenberger Location: REM-3B61#2C18

Art Unit: 1635

Thursday, September 15, 2005

Case Serial Number: 10/721693

From: Mary Jane Ruhl

Location: Biotech-Chem Library

Remsen 1-A-62

Phone: 571-272-2524

maryjane.ruhl@uspto.gov

Search Notes

Examiner Wollenberger,

Here are the results for your recent search request.

Please feel free to contact me if you have any questions about these results.

Thank you for using STIC services. We appreciate the opportunity to serve you.

Sincerely,

Mary Jane Ruhl Technical Information Specialist STIC Remsen 1-A-62 Ext. 22524



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STIG-Biotech/ChemLib

65030

From:

Wollenberger, Louis V.

Sent:

Wednesday, September 07, 2005 2:32 PM

To: Subject:

STIC-Biotech/ChemLib Sequence search request

September 7, 2005

Re: Patent Application No. 10/721,693

offe

Please carry out the following sequence searches for the above identified application:

- 1. A length limited search of oligonucleotide SEQ ID NO:1, where the lower limit is 15 and the upper limit is 30.
- 2. A length limited search of oligonucleotide SEQ ID NO:2, where the lower limit is 15 and the upper limit is 30.

Thanks, Louis Wollenberger Examiner, Art Unit 1635 REM-3B-61, Mailbox 2C-18 x2-8144

STAFF USE ONLY

Searcher:_____
Searcher Phone: 2Date Searcher Picked up:____
Date Completed:____
Searcher Prep/Rev. Time:___
Online Time:____

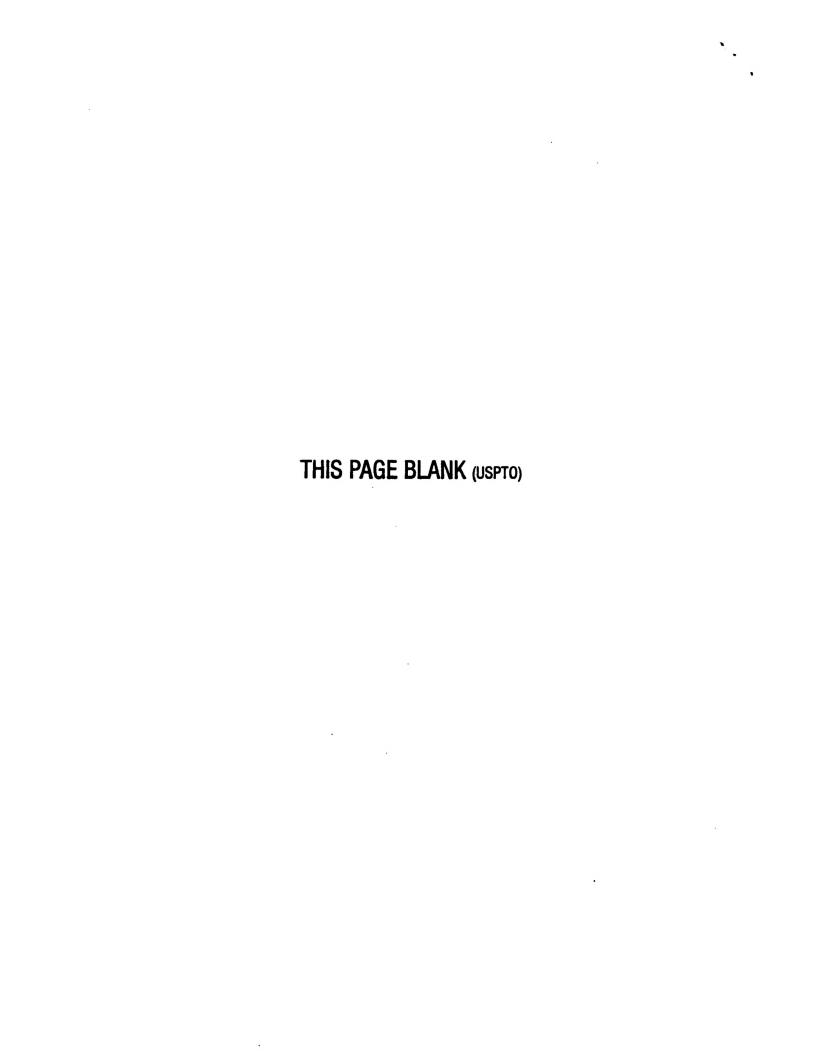
Type of Search

NA#:____ AA#:___
Interference: SPDI:__
S/L: Oligomer:__
Encode/Transl: Text:__
Structure#:___ Text:__
Inventor:___ Litigation:___

Vendors and cost where applicable STN:______
DIALOG:_____
QUESTEL/ORBIT:______

LEXIS/NEXIS:_____SEQUENCE SYSTEM:______
WWW/Internet:_____

Other(Specify):_



Sep 15 14:29:24 2005

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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.

Copyright

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September 12, 2005, 16:58:36; Search time 278.5 Seconds (without alignments) 495.196 Million cell updates/sec
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Sequence 4, 7
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Sequence 1, 7
Sequence 1, 7
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1. (egn2_6/ptodata/1/pubpna/USO7_NEW_PUB.Beq:*

1. (egn2_6/ptodata/1/pubpna/USO6_NEW_PUB.Beq:*

1. (egn2_6/ptodata/1/pubpna/USO6_NEW_PUB.Beq:*

1. (egn2_6/ptodata/1/pubpna/USO7_NEW_PUB.Beq:*

1. (egn2_6/ptodata/1/pubpna/USO8_NEW_PUB.Beq:*

1. (egn2_6/ptodata/1/pubpna/USO8_NEW_PUB.Beq:*

1. (egn2_6/ptodata/1/pubpna/USO8_PUBCOMB.Beq:*

1. (egn2_6/ptodata/1/pubpna/USO8_PUBCOMB.Beq:*

1. (egn2_6/ptodata/1/pubpna/USO9_NEW_PUB.Beq:*

1. (egn2_6/ptodata/1/pubpna/USO9_NEW_PUB.Beq:*

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2. (egn2_6/ptodata/1/pubpna/USO09_NEW_PUB.Beq:*

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2. (egn2_6/ptodata/1/pubpna/USO09_NEW_PUB.Beq:*

2. (egn2_6/ptodata/1/pubpna/USO09_BUBCOMB.Beq:*

2. (egn2_6/ptodata/1/pubpna/USO08_BUBCOMB.Beq:*

2. (egn2_6/ptodata/1/pubpna/USO08_BUBCOMB.Beqg:*

2. (egn2_6/ptodata/1/pubpna/USO08_BUBCOMB.Beqg:*

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US-10-852-997-2

US-10-852-997-2

US-10-852-997-4

US-10-721-693-1

US-10-721-693-1

US-10-852-997-1
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nucleic search, using sw model
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Maximum DB seq length: 30
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Sequence 2, Application US/10721693

Publication No. US20040162255A1

GENERAL INFORMATION:
APPLICANT: Meditronic, Inc.
TITLE OF INVENTION: Treatment of Neurodegenerative Disease Through Intracranial Deliv
TITLE OF INVENTION: SIRNA
TITLE OF INVENTION: BIRNA
TITLE OF INVENTION: BIRNA
CURRENT APPLICATION NUMBER: US/10/721,693
CURRENT PILING DATE: 2003-11-25
NUMBER OF SEQ ID NOS: 23
                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
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Gaps

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Score 21; DB 19; Length 21; Pred. No. 0.0072; Mismatches 0; Indels

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Query Match
100.0%;
Best Local Similarity 100.0%;
Matches 21; Conservative 0.

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APPLICANT: Kaemmerer, William F.
TITLE OF INVENTION: Treatment of Neurodegenerative Disease Through Intracranial Delive
TITLE OF INVENTION: SIRNA
FILE REFERENCE: P11089.00
CURRENT APPLICATION NUMBER: US/10/721,693
CURRENT FILING DATE: 2003-11-25
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 21
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Publication No. US20040162255A1
Publication No. US20040162255A1
GENERAL INFORMATION:
APPLICANT: Medironic, Inc.
APPLICANT: Medironic, Inc.
TITLE OF INVENTION: Freatment of Neurodegenerative Disease Through Intracranial Delive
TITLE OF INVENTION: SIRNA
FILE REPERENCE: 101089.00
CURRENT APPLICATION NUMBER: US/10/721,693
CURRENT FILING DATE: 2003-11-25
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 21
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Pred. No. 0.0072;
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0.12;
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PRIOR APPLICATION NUMBER: 10/721,693
PRIOR FILING DATE: 2003-11-25
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
LENGTH: 21
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US-10-721-693-1/c
Sequence 1, Application US/10721693
Publication No. US20040162255A1
GENERAL INFORMATION:
APPLICANT: Medtronic, Inc.
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; ORGANISM: Homo sapiens
US-10-852-997-4
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ORGANISM: Homo sapiens
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Matches 21; Conserv
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Matches 19; Conserv
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APPLICANT: Medtronic, Inc.
APPLICANT: Kaemmerer, William F.
APPLICANT: Kaemmerer, William F.
APPLICANT: Kaemmerer, William F.
TITLE OF INVENTION: SIRNA
FILE REFERENCE: P11089.00
CURRENT APPLICATION UNMER: US/10/721,693
CURRENT FILING DATE: 2003-11-25
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin version 3.1
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APPLICANT: Meditonic, Inc.
APPLICANT: Kaemmerer, William F.
APPLICANT: Kaemmerer, William F.
TITLE OF INVENTION: Treatment of Neurodegenerative Disease Through Intracranial Deliv
TITLE OF INVENTION: aikna
FILE REFERENCE: P11089.02
CURRENT APPLICATION NUMBER: US/10/852,997
CURRENT FILING DATE: 2004-05-25
PRIOR APPLICATION NUMBER: 10/721,693
PRIOR FILING DATE: 2003-11-25
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.1
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Publication No. US20040220132A1

GENERAL INFORMATION:

APPLICANT: Medtronic, Inc.

APPLICANT: Medtronic, Inc.

APPLICANT: Medtronic, Inc.

TITLE OF INVENTION: Treatment of Neurodegenerative Disease Through Intracranial Deliverine of Invention with the part of Invention of Inventi
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                              Sequence 4, Application US/10721693
Publication No. US20040162255A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/10852997; Publication No. US20040220132A1; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-721-693-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 21; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 4
LENGTH: 21
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LENGTH: 21
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Sequence 272193. Application Wo. US20050026164A1

GENERAL INFORMATION:

APPLICANT: Xue Mei Zhou

TITLE OF INFORMATION:

FILE REFERENCE: 3528.1

CURRENT APPLICATION NUMBER: US/10/719,900

CURRENT FILING DATE: 2003-11-20

PRIOR FILING DATE: 2002 11 20

NUMBER OF SEQ ID NOS: 982914

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25
                 TITLE OF INVENTION: Methods of Genetic Analysis of Mouse FILE REFERENCE: 3528.1

CURRENT APPLICATION NUMBER: US/10/719,900

CURRENT FILING DATE: 2003-11-20

PRIOR APPLICATION NUMBER: 60/427,808

PRIOR FILING DATE: 2002 11 20

NUMBER OF SEQ ID NOS: 982914

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 569157

LENGTH: 25
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TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11.20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 49468
LENGTH: 25
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Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 13; Conservative 0; Mismatches 0;
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Pred. No. 1.9e+03;
0; Mismatches 0;
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Publication No. US20050026164A1
GENERAL INFORMATION:
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Best Local Similarity 100.0%;
Matches 12; Conservative 0
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US-10-719-900-569157
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US-10-719-900-49468
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; ORGANISM: Mus musculus
US-10-719-900-272193
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APPLICANT: Medironic, Inc.
APPLICANT: Kaemmerer, William F.
APPLICANT: Kaemmerer, William F.
TITLE OF INVENTION: Treatment of Neurodegenerative Disease Through Intracranial Deliv
TITLE OF INVENTION: SIRNA
PILE REFERENCE: P11089.02
CURRENT APPLICATION NUMBER: US/10/852,997
CURRENT FILING DATE: 2004-05-25
PRIOR APPLICATION NUMBER: 10/721,693
PRIOR FILING DATE: 2003-11-25
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.1
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APPLICANT: Meditionic, Inc.
APPLICANT: Kaemmerer, William F.
TITLE OF INVENTION: Treatment of Neurodegenerative Disease Through Intracranial Deliv
TITLE OF INVENTION: SIRNA
FILE REFERENCE: P11089.02
CURRENT APPLICATION NUMBER: US/10/852,997
CURRENT FILING DATE: 2004-05-25
PRIOR APPLICATION NUMBER: 10/721,693
PRIOR FILING DATE: 2003-11-25
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.1
SEQ ID NO 3.1
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0.12;
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100.0%; Pred. No. ...
0; Mismatches
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US-10-719-900-569157
; Sequence 569157
; Publication No. US20050026164A1
; GENERAL INFORMATION:
                                                                                                                                         ; Sequence 1, Application US/10852997; Publication No. US20040220132A1; GENERAL INFORMATION: APPLICANT: Meditronic, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/10852997
Publication No. US200400220132A1
GENERAL INFORMATION:
APPLICANT: Medironic, Inc.
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21 TTCGTTGCTCCGCTCTTGG
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CORGANISM: Homo sapiens
US-10-852-997-1
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CORGANISM: Homo sapiens
US-10-852-997-3
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Best Local Similarity
Matches 19; Conserva
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Best Local Similarity
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US-10-852-997-3/c
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                                                                                                                                                                                                                                               Sequence 399511, Application US/10719900
| Publication No. US20050026164A1
| GENERAL INFORMATION:
| APPLICANT: Xue Mei Zhou
| TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
| TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
| TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
| TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
| CURRENT APPLICATION WUMBER: US/10/719,900
| CURRENT FILING DATE: 2003-11-20
| PRIOR FILING DATE: 2002-11-20
| NUMBER OF SEQ ID NOS: 982914
| SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
| LENGTH: 25
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; Publication No. US2005002616431
; GENERAL INFORMATION:
    APPLICANT: Kue Mei Zhou
    TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REPERENCE: 3520.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR APPLICATION NUMBER: 60/427,808
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 911843
57.1%; Score 12; DB 21; Length 25; 100.0%; Pred. No. 1.9e+03; ive 0; Mismatches 0; Indels
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; Sequence 911844, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 12; Conservative
  Query Match
Best Local Similarity 100.
Matches 12, Conservative
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Best Local Similarity 100.
Matches 12; Conservative
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ORGANISM: Mus musculus
US-10-719-900-399511
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US-10-719-900-399511/c
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APPLICANT: Xue Mei Zhou

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TITLE OF INVENTION: Methods of Genetic Analysis of Mouse FILE REFERENCE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 911844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 950357
LENGTH: 25
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PUblication No. US20050026164A1
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT APPLICATION NUMBER: 60/427,808
PRIOR PILING DATE: 2002.11.20
PRIOR FILING DATE: 2002.11.20
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Job time : 279.5 secs
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Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                            12; Conservative
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US-10-719-900-911844
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US-10-719-900-950357
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Best Local Similarity
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US-10-719-900-950357/c
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September 12, 2005, 15:58:45; Search time 1377.5 Seconds (without alignments) 580.290 Million cell updates/sec
      GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                         nucleic search, using sw model
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Gapop_60.0 , Gapext 60.0
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21
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Title: Perfect score:

Sequence:

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Run on:

Scoring table:

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1M00202J03
2M0107P11
2ML1 1028
5009-0-41
5009-0-41
5009-0-18
5009-0-18
5009-0-18
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5009-0-18
1M0324C10
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BM398612 CF3376170 CF337647 AZ326642 AZ326642 AZ423444 BM398108 BM398108 BM398108 BM398108 BM398108 BM398108 AZ822792 AZ822792 BM399528 BM399528 BM399538 AZ491197 AZ502375 AZ502375 AZ502375 AZ502375

BM399170 AZ32643 AZ32644 AZ423444 AZ42383 BM390353 BM398106 BM398106 BM398156 BM39253 AZ593454 AZ82239 BM399525 BM399525 AZ5931954 AZ468735 AZ468735 AZ468735 AZ468735 AZ468735 AZ468735 AZ468735 AZ468735 AZ468735 AZ468735

Total number of hits satisfying chosen parameters:

0

Word size :

Searched:

Post-processing: Listing first

Database:

Minimum DB seq length: 15 Maximum DB seq length: 30

ALIGNMENTS

RESULT 1	a Mu	25 5p DNA 1119027E01.2EL y2 1119 - RescueMu Grid AA Zea mays g	survey sequence.	ON CG712540	VERSION CG712540.1 GI:37738446	KEYWORDS GSS	SOURCE Zea mays	ORGANISM Zea mays		Charmatorhyta . Marmoliophyta . Doales Dhareae . Dhareae	clade: Panicoideae: Andropoconeae: Zea	REFERENCE 1 (bases 1 to 25)	AUTHORS Walbot, V.	TITLE Maize genomic sequences found using engineered RescueMu transposon			Stanford University	855 California Ave, Palo Alto, CA 94304, USA	Tel: 650 723 2227	Fax: 660 725 8221	Demont: Wathorewording and the Control of the Contr	Possible ligation site of ends cut by 4 different endonucleases. Reverse complemented nost-ligation semisore from source semisore	Date: 119027 70w: F column: 01	FEATURES Location/Oualifiers	rce 1	/organism="Zea mays"	/mol_type="genomic DNA"	/cultivar="mixed background W23/A188/B73/K55"	/db_xref="taxon:4577"	/tissue_type="leaf"	/dev_stage="adult"	/lab_host="DH10B"	/clone lib="1119 - RescueMu Grid AA"	/note="Organ: leaf; Vector: RescueMu (engineered from	pBlueScript backbone); Site 1: BamHI; Site 2: BqlII;	RescueMu is a 4.9 kb, modified maize Mu transposon	designed to allow plasmid rescue from total genomic DNA.	Mu elements insert preferentially into transcription	units. For more information on RescueMu, go to the web	site 'www.zmdb.jastate.edu' and follow the links for	COCCO TO THE PROPERTY OF THE P
													Pred. No. is the number of results predicted by chance to have a	greater than or equal to the score of the result being printed,	re discribación:				Description		·	X604/3 \$NI3906.E1						BZ765015 SALK_1278						BM398968 5009-0-51	AZ637794 1M0497D20	AZ992248 2M0276N17		BM398994 5009-0-51	CF333123 JMT01-0		-
	processing: Listing first 45 summaries												of results predicte	score greater than or equal to the score of		SUMMARIES			DB ID	0.00010000	200717			 9 AJ597633	4 BM399181	·							4 BM398964		8 AZ637794	8 AZ992248	4 BM397402	4 BM398994	7 CF333123	8 AZ636817	
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
Hillier,L., Clark).
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence starts: 1
High quality sequence stops: 1
Source: INAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (lift@eimage.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                   19 mRNA linear EST 24-MAY shear EST 24-MAY shinear EST 24-MAY shilg06.rl Soares infant brain INIB Homo sapiens cDNA clone IMAGE:43057 5' similar to SP:SYNP_RAT P22831 ;, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                            47.6%; Score 10; DB 9; Length 25;
100.0%; Pred. No. 1e+05;
cive 0; Mismatches 0; Indels
                                                                                              Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="73 days post_natal"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares infant brain INIB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .28
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/db_xref="GDB:415598"
/db_xref="taxon:9606"
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High quality sequence stop: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (human)
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                                                                                                                                 10, Conservative
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Best Local Similarity
Matches 10; Conservat
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Length 28;

47.6%; Score 10; DB 7; 100.0%; Pred. No. 1e+05;

Query Match Best Local Similarity

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musculus C5/Bu/60 (maie, was concerned laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarces gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil/473214/gb/R729072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1) (bases 1) (
                                                                                                                                                                                                                                                                                                                                                                      AZ599480
1M0414C20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic Cone UUGC1M0414C20 R, genomic survey sequence.
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Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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/clone lib="Mouse 10kb plasmid UUGCNM library."
/note="Vector: PWD42ry; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Seq primer: CACACAGGAAACAGCTATGACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
/strain="C57BL/6J"
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Location/Qualifiers
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Insert Length: 10000 Std Erro
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Mus musculus
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Fax: 801 585 7177
     16
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7 TTGCTCCGCT
                                                                                                         15 Trecreecr
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Matches

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AJ593450 LOCUS

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REFERENCE AUTHORS

JOURNAL MEDLINE

TITLE

PUBMED

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (Dases 1 to 22)

2 Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

LD Unpublished (2001)

Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/mol_type="genomic DNA"
/ecctype="COl-0"
/db xref="taxon:3702"
/clone="SALK_107640.42.05.x"
/clone="SALK_107640.42.05.x"
/clone="FCR was performed on Arabidopsis thaliana lines each of which contains on on arabidopsis thaliana lines each of which contains on or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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GSS; left border; T-DNA flanking sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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T-DNA integration into the Arabidopsis genome depends on sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AJ597633 15-JAN-20
Arabidopsis thaliana T-DNA flanking sequence, left border, clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 5' end of At3g33595.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0, Indels
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                                                                                        Arabidopsis thaliana (thale cress)
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EMBO Rep. 3 (12), 1152-1157 (2002)
22363535
12446565
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                              BH905710.1 GI:22718643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: ecker@salk.edu
                                                                                                                   Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Class: TDNA tagged
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AATTCGTTG 18
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AJ597633
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Submitted (23-OCT-2003) Balzergue S., UWRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evy cedex, FRANCE
Gaston Cremieux, 91057 Evy cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program "Genoplante" (http://www.genoplante.com and http://genoplante-info.infoiogen.fr).
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                                                                                                                                                                                                                                                          AJ593450 20 bp DNA linear GSS 15-JAN-2004
Arabidopsis thaliana T-DNA flanking sequence, left border, clone
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EMBO Rep. 3 (12), 1152-1157 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryoča, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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GSS; left border; T-DNA flanking sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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/mol_type="qenomic DNA"
coltivar="Wassillewskija"
/db_xref="taxon:3702"
/clone="380P06"
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    .20
    /note="T-DNA flanking sequence"

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Balzergue, S.
9; Conservative
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GSS 15-JAN-2004

Query Match

FEATURES

Matches

DEFINITION

RESULT 5 · BH905710 LOCUS

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RESULT 8
AZ861916/c
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                                                           Submitted (13-00T-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Ery cedex, FRANCE
Gaston Cremieux, 91057 Ery cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versaillee). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at thtps://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante-inf(http://www.genoplante.com and Location/Qualifiers)
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/strain="CU428.1"
/db xref="texon:5911"
/clone lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: BlueScript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone_lib="Arabidopsis thaliana T-DNA insertion lines"
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Errankel, J. and Klobutcher, L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells Unpublished (2002)
Contact: Turkwwitz AP
Molecular Genetics and Cell Biology
University of Chicago, IL 60637, USA
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Tetrahymena thermophila
Bukaryota, Alveolata, Ciliophora, Oligohymenophorea,
Hymenostomatida, Tetrahymenina, Tetrahymeniae,
I (bases 1 to 25)
Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25 bp mRNA linear EST 17 1009-0-54-F03.t.1 Chilcoat/Turkewitz cDNA (large fraction) Tetrahymena thermophila cDNA, mRNA sequence. BM399181
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/mol_type="genomic DNA"
/cultivar="Wassillewskija"
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    .24
/note="T-DNA flanking sequence"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:3702"
/clone="454D02"
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Best Local Similarity 100.
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                     Balzergue, S.
Direct Submission
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16 AATTCGTTG 24
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gilfyla) [AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XII.0-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                   AZ861916
2M0168K17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0168K17 R, genomic survey sequence.
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Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 30)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Museam, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.,
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
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84112, USA
                                                                  Gaps
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                                                               Indels
42.9%; Score 9; DB 4; Length 25; 100.0%; Pred. No. 4.5e+05;
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Insert Length: 10000 Std Brror: 0.00
Plate: 0168 row: K column: 17
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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                                                               0; Mismatches
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organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0168K17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 30.
Location/Qualifiers
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                                                                  9; Conservative
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Fax: 801 585 7177
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                               Best Local Similarity
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Class: TDNA tagged.
Location/Qualifiers
BZ765015
BZ765015.1 GI:28937568
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Fax: 858 558 6379
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BM398577.1 GI:18198630
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/clone lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alongo,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Sanina,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
The Salk Institute for Biological Studies
Tels 858 453 4100 x1752
Fax: 858 558 6379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: ecker@aalk.edu
This is single pass sequence recovered from the left border of TDNA.
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                                   DB 8; Length 30; 0.4.5e+05; ches 0; Indels
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/mol_type="genomic DNA"
/ecotype="Col-0"
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                                   42.9%; Score 9; DB 8
100.0%; Pred. No. 4.5
:ive 0; Mismatches
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Arabidopsis thaliana
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Location/Qualifiers
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                                                                                                                                                         1. (bases 1 to 30)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
Murabidopsis Genome
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Bological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
                                                                 Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db xref="taxon:3702" / db xref="taxon:3702" / clone="SALK 127827.19.55.x" / clone="SALK 127827.19.55.x" / clone lib="Ārabidopsis thaliana TDNA insertion lines" / note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (Dases 1 to 18)

Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.

BST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This is single pass sequence recovered from the left border of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
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Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
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920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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FEATURES

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BM397580 20 bp mRNA linear EST 17-JAN-2002 5009-0-34-G11.t.1 Chilcoat/Turkewitz cDNA (large fraction) Tetrahymena thermophila cDNA, mRNA sequence.
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/clone lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: BlueScript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
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Tetrahymena thermophila
Bukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Bukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
1 (bases 1 to 20)
Turkewitz,A.D., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
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Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankelj.J. and Klobutcher,L.
BST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
                                                                                                                                                                                                                                      Tetrahymena thermophila
Eukaryota, Alveolata, Ciliophora, Oligohymenophorea,
Hymenostomatida, Tetrahymenina, Tetrahymena.
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/mol_type="mRNA"
/strain="CU428.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     University of Chicago
920 E. Sath Street, Chicago, IL 60637, USA
7TE1: 773 702 4374
Fax: 773 702 3172
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Tel: 773 702 4374
Fax: 773 702 3172
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                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Turkewitz AP
Molecular Genetics and Cell Biology
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Location/Qualifiers
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7LEAF--03-D20.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--03-D20, mRNA
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/clone lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: BlueScript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza,
I (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yonglin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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/db_xref="taxon:39947"
/clone="TubAF-03-D20"
/tissue_type="leaf" days after germination"
/dev_stage="7 days after
/lab host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/clone_lib="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
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|mol_type="mRNA"
|cultivar="Nackdong"
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                                                                                            organism="Tetrahymena thermophila"
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100.0%; Pred. No. 1.9
cive 0; Mismatches
Email: apturkew@midway.uchicago.edu
                Seq primer: T3.
Location/Qualifiers
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                                                                                                               /mol_type="mRNA"
/strain="CU428.1"
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Best Local Similarity 100.
Matches 8; Conservative
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Matches 8; Conserv
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ACCESSION VERSION KEYWORDS SOURCE REFERENCE AUTHORS

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Gaps

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BM398964 2002 20 bp mRNA linear EST 17-JAN-2002 5009-0-51-B10.t.1 Chilcoat/Turkewitz cDNA (large fraction) Tetrahymena thermophila cDNA, mRNA sequence.
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                                                                                         /db_xref="taxon:5911"
/clone lib="Chilcoat/Turkewitz cDNA (large fraction)"
/clone="Vector: BlueScript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
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preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
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Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Busaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.

1 (bases 1 to 20)
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E.,
Frankel, J. and Klobutcher, L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
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38.1%; Score 8; DB 4; Length 20;
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Matches 8; Conservative 0; Mismatches 0; Indels
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Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
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BM398964.1 GI:18199017
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Search completed: September 12, 2005, 18:09:00 Job time : 1379.5 secs

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AX497756 Sequence
AX822200 Sequence
AX825860 Sequence
A51886 Sequence 3
A52459 Sequence 3
A52459 Sequence 3
AR111715 Sequence
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AR299168 Sequence
AR319109 Sequence
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AX36185 Sequence
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Treatmerer, W.F.
Treatment of neurodegenerative disease through intracranial delivery of sirna
Patent: W0 2004047872-A 1 10-JUN-2004;
Medtronic, Inc. (US)
Location/Qualifiers
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Pred. No. 0.75;
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Sequence 3 from Patent W02004047872.
CQ824576.1 GI:49021596
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Sequence 1 from Patent WO2004047872.
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AR315108
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CQ824574.1 GI:49021592
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Best Local Similarity 100.0%;
Matches 21; Conservative 0;
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AR469952 Sequence
AR053175 Sequence
AR09819 Sequence
BD195066 Catalytic
AR228457 Sequence
AR227453 Sequence
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AR327453 Sequence
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AX73229718 Sequence
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Sequence
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AR442594 Sequence
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          GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                  4708233 segs, 24227607955 residues
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                                              - nucleic search, using sw model
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(C12R5/10, C12R1:91), (C12P21/02, C12R1:91), (C12P21/02, C12R1:19),
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C12N15/09,A61K35/74,A61K35/76,A61K38/00,A61K38/00,A61K48/00, PC
C07K14/47,
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Katsuhiko, M., Jun, A., Kenji, N. and Katsunori, N. Neurogenesia-inductive gene
Parent: JP 199341985-A 28 14-DEC-1999;

RIKAGAKU KENKYUSHO
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Location/Qualifiers
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9.3;
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Neurogenesis-inductive gene.
E30575
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               Location/Qualifiers
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Strandedness: Single,
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14-DEC-1999
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JP 199341985-A/28.
unidentified
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Medtronic, Inc. (US)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Treatment of neurodegenerative disease through intracranial delivery of sirna Patent: WO 200447872-A 2 10-JUN-2004; Medtronic, Inc. (US)
Location/Qualifiers
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Treatment of neurodegenerative disease through intracranial
delivery of stram
Patent: WO 2004047872-A 4 10-JUN-2004;
                                               Kaemmerer,W.F.

Treatment of neurodegenerative disease through intracranial delivery of sirna
Patent: WO 2004047872-A 3 10-JUN-2004;
Medtronic, inc. (US)
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Seguence 2 from Patent WO2004047872.
CQ824575
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Homo sapiens
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ive 0; Mismatches 0;
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I (bases 1 to 20)

Kim,C.M., Park,H.K. and Jang,H.J.

Oligonuclectide for detection and identification of Mycobacteria

Patent: US 6670130-A 202 30-DEC-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unclassified.

I (bases 1 to 22)
Costa,M.R., Doberstein,S.K., Elson,S.L., Ferguson,K.C. and Homburger,S.A.
Animal models and methods for analysis of lipid metabolism and screening of pharmaceutical and pesticidal agents that modulate lipid metabolism
Patent: US 6781028-A 81 24-AUG-2004;
Location/Qualifiers
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                                                   1 (bases 1 to 20)
Mikoshiba.K., Aruga,J., Nagai,T. and Nakata,K.
Neurogenesis inducing genes
Patent: US 6506637-A 31 31-DEC-2002;
Location/Qualifiers
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Seguence 202 from patent US 6670130.
AR42594
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Sequence 81 from patent US 6781028.
AR568156
AR568156.1 GI:53986443
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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1 (bases 1 to 29)
Orr,H T., Ranum,L.P.W., Chung,M.-y. and Zoghbi,H.Y.
Gene sequence for spinocerebellar ataxia type 1 and method for diagnosis
Patent: 10.834183-A 81 10-NOV-1998;
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52.4%; Score 11; DB 6; Length 25; 100.0%; Pred. No. 2.2e+05; ive 0; Mismatches 0; Indels
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AX469952 25 bp D
Seguence 69 from Patent WO02053771.
AX469952
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Sequence 81 from patent US 5834183.
AR053175.1 GI:5978037

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AR328457.1 GI:33714265
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Best Local Similarity 100.
Matches 10; Conservative
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AR327452
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AR243693
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Unclassified.
1 (bases 1 to 30)
1 (bases 1 to 30)
Deibel, M.R. Jr., Yem, A.W. and Wolfe, C.L.
Catalytic macro molecules having cdc25B like activity
Patent: US 6074851-A 42 13-UNN-2000,
                                                                                                                                                                                                                                                                                                                                      30 bp DNA linear
Catalytic polymer having CDC25B like activity.
BD195066
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Jr,M.R.D., Yem,A.W. and Wilson,C.L.
Catalytic polymer having CDC25B like activity
Patent: JP 2002515742-A 27 28-MAY-2002;
PARMACIA & UPJOHN CO
OS Unidentified
                   Sequence 42 from patent US 6074851.
                                                                                                                                                                              /organism="unknown"
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Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Bscobedo, J.
Pathod and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor Patent: US 6566127-A 5859 20-MAY-2003;
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Unclassified.
1 (basea to 17)
Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
Method and reagent for the treatment of diseases or conditions
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Use of a vector expressing DNA polymerase .beta. as medicine Patent: US 6475596-A 5 05-NVV-2002;
Location/Qualifiers
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Sequence 4854 from patent US 6566127.
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AR327452.1 GI:33713260
Sequence 5859 from patent US 6566127.
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Best Local Similarity 100.0%; Pred. No. 8.2e+05;
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1 aattcgttgctccgctcttgg 21 Sequence:

OLIGO_NUC Gapop_60.0 , Gapext 60.0 Scoring table:

1202784 segs, 818138359 residues Searched:

0 Word size :

914340 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 15 Maximum DB seq length: 30

Post-processing: Listing first 45 summaries

Database :

Issued Patents NA:*

(cgn2_6/ptodata/1/ina/5A_COMB.seq:*

(cgn2_6/ptodata/1/ina/5B_COMB.seq:*

(cgn2_6/ptodata/1/ina/6A_COMB.seq:*

(cgn2_6/ptodata/1/ina/6B_COMB.seq:*

(cgn2_6/ptodata/1/ina/Redia/seq:*

(cgn2_6/ptodata/1/ina/Redia/seq:*

(cgn2_6/ptodata/1/ina/Redia/seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMADIES

SUMMARIES	ID Description	US-09-332-522E-81 Sequence 81, Appl		31,	US-09-342-325C-31 Sequence 31, Appl	202	Sequence 2, 1	PCT-US93-12078-3 Sequence 3, Appli	Sequence 140		396-196G-18110	96G-18111 Sequence 1811	99	6642	99	42	9	2 Sequence 22	m	53	-452A-5645 Seguence 5645	5646	11,	US-10-023-649A-19 Sequence 19, Appl	22,	US-08-793-044-7 Sequence 7, Appli	.16 Sequence 16,	
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	Query Match Length DB	22	20	20	20	20	22	22	25	25	25	25	25	25	25	30	30	18	20	20	20	20	20	20	21	22	23	
d	Query Match	57.1	52.4	52.4	52.4	52.4	52.4	52.4	52.4	52.4	52.4	52.4	52.4	52.4	52.4	52.4	52.4	47.6	47.6		47.6	47.6	•	47.6	47.6	٠	47.6	
	Score	12	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	10	10	10	10	10	10	10	10	10	10	
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Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	
US-09-270-767-62514	US-08-379-926A-4	US-08-866-446-1	US-09-396-196G-12977	US-09-396-196G-12978	US-09-396-196G-34741	US-09-396-196G-52807	US-09-396-196G-52808	US-09-396-196G-52809	US-09-396-196G-56973	US-09-396-196G-73270	US-09-396-196G-73271	US-09-396-196G-77212	US-09-396-196G-87841	US-09-396-196G-96977	US-09-396-196G-96978	US-09-396-196G-96979	US-09-396-196G-96980	O HINGS AND A TK
4	٦	m	4	4	4	4	4	4	4	4	4	4	4,	4	4	4	4	
24	25	25	25	25	25	25	25	25	25	25	25	25	25	25	25	25	25	
47.6	47.6	47.6	47.6	47.6	47.6	47.6	47.6	47.6	47.6	47.6	47.6	47.6	47.6	47.6	47.6	47.6	47.6	
10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	
28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	
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ALIGNMENTS

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APPLICANT: COSTA, M.
APPLICANT: COSTA, M.
APPLICANT: Doberstein, S.
APPLICANT: Blson, S.
APPLICANT: Elson, K.
APPLICANT: Blson, K.
APPLICANT: Britan, S.
APPLICANT: Homberger, S.
TITLE OF INVENTION: ANIMAL MODELS AND METHODS FOR ANALYSIS OF LIPID METABOLISM AND S.
TITLE OF INVENTION: OF PHARMACEUTICAL AND PESTICIDAL AGENTS THAT MODULATE LIPID META
CURRENT APPLICATION NUMBER: US/09/332,522E
CURRENT APPLICATION NUMBER: US/09/332,522E
CURRENT FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 95
SOFTWARE: PATENT OF SEQ ID NOS: 95
SOFTWARE: PATENT OF SEQ ID NOS: 95
LENGTH: 22
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; Batent No. 6066460
; GENERAL INFORMATION:
APPLICANT: Kirschner, Mark W.
; APPLICANT: Kirschner, No. 6066460iyuki
; TITLE OF INVENTION: METHOD FOR CLONING SECRETED PROTEINS
; FILE REFERRINCE: HAV-022.01
; CURRENT APPLICATION NUMBER: US/09/121,920
; CURRENT FILING DATE: 1998-07-24
; EARLIER APPLICATION NUMBER: 60/053,586
; SARLIER FILING DATE: 1998-07-24
; WUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 22,
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Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 12; Conservative 0; Mismatches 0;
                      Sequence 81, Application US/09332522E
Patent No. 6781028
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-332-522E-81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                              Length 20;
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                                                                                                                                                       0; Indels
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Patent No. 650057;
GENERAL INFORMATION:
APPLICANT: Mikoshiba, Kateuhiko
APPLICANT: Aruga, Jun
APPLICANT: Aruga, Jun
APPLICANT: Aruga, Jun
APPLICANT: Resunci, Takeharu
APPLICANT: Kateunci, Nakata
TITLE OF INVENTION: Neurogenesis Inducing Gene
FILE REFRENCE: HIRAKI-03814
CURRENT APPLICATION NUMBER: US/09/342,325C
CURRENT FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: JP98/86979
PRIOR FILING DATE: 1998-03-31
PRIOR FILING DATE: 1998-03-31
PRIOR FILING DATE: 1998-04-30
PRIOR FILING DATE: 1998-04-30
PRIOR FILING DATE: 1998-04-30
PRIOR FILING DATE: 1998-05-28
NUMBER OF SEQ ID NOS: 64
SEQ ID NO 31
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Michoshiba, Katsuhiko
APPLICANT: Aruga, Jun
APPLICANT: Nagai, Takeharu
APPLICANT: Nakaia, Rateunori
TITLE OF INVENTION: Neurogenesis Inducing Gene
FILE REFERENCE: Hirak-03497
CURRENT APPLICATION NUMBER: US/09/172,045
CURRENT FILING DATE: 1998-10-08
EARLIER APPLICATION NUMBER: JP98/86979
EARLIER APPLICATION NUMBER: JP98/86979
EARLIER APPLICATION NUMBER: JP98/121456
EARLIER APPLICATION NUMBER: JP98/121456
EARLIER PILING DATE: 1998-04-30
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 31
LENGTH: 20
                                                                                                            Score 11; DB 3;
Pred. No. 2e+03;
                                                                                              52.4%; Scc. 100.0%; Pred. No. 2. ... 0; Mismatches
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Patent No. 6277594
GENERAL INFORMATION:
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                                                                                                            Query Match
Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                                                                                                                                    11 CTCCGCTCTTG 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: primer
US-09-121-920-26
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US-09-342-325C-31/c
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US-09-172-045-31/c
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MESULY: 5-
US-005-202
US-005-202
Sequence 202, Application US/09980052
Facent No. 6670130
GENERAL INFORMATION:
APPLICANT: KIM, Jeong Joon; SJ HIGHTECH Co., Ltd.
APPLICANT: KIM, Cheol Min
APPLICANT: RIM, Cheol Min
FILE REFERENCE: PP05020/PCT
CURRENT APPLICATION NUMBER: KR 10-1999-0019631
PRIOR APPLICATION NUMBER: KR 10-1999-0019632
PRIOR PLING DATE: 1999-05-29
PRIOR PLING DATE: 1999-05-29
PRIOR PLING DATE: 1999-05-29
PRIOR PLING DATE: 1999-06-29
PRIOR PPLING DATE: 1999-06-29
PRIOR PLING DATE: 1999-05-29
PRIOR PLING DATE: 1999-05-29
PRIOR PLING DATE: 1999-05-29
PRIOR PLING DATE: 1999-06-29
PRIOR PLING DATE: 1999-06-39
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                                                                                             ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-342-325C-31
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                                                                                                                                                                                             Length 20;
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                                                                                                                                                                                          Query Match 52.4%; Score 11; DB 4; Length 20; Best Local Similarity 100.0%; Pred. No. 2e+03; Matches 11; Conservative 0; Mismatches 0; Indels
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COUNTRY: United States of America
POSTAL CODE: 78701
TELEPHONE NO: (512)499-4462
TELEPAX: (512)499-4523
TELEPAX: (512)499-4523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 201 West 7th Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application PC/TUS9312078 GENERAL INFORMATION:
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Austin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                    10 CICCGCICITG 20
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APPLICANT: TELEPHONE
APPLICANT: TELEFAX:
TITLE OF INVENTION:
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SYSTEM
STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCT-US93-12078-2/c
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 22;
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Sequence 14051, Application US/09396196G

Sequence 14051, Application US/09396196G

Patent No. 6821724

GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart

APPLICANT: David Lockhart

TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1

CURRENT APPLICATION NUMBER: US/09/396,196G

CURRENT FILING DATE: 1999-09-15

PRIOR FILING DATE: 1999-09-15

NUMBER OF SEQ ID NOS: 127806

SEQ ID NO 14051

LENGTH: 25
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100.0%; Pred. No. 2e+03;
cive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                    COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12078
FILING DATE: UNKNOWN
CLASSIFICATION NUMBER: 07/992,900
FILING DATE: 16.12.92
ATTORNEY/AGENT INFORMATION:
NAME: HODGINS: DANTEL S.
REGISTRATION NUMBER: 31,026
REFERENCE/DOCKET NUMBER: UTFP046PCT
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION SP0-2676
TELESPANS: 713-789-2676
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 DASE pairs
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Pred. No.
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; Sequence 18109, Application US/09396196G
; Parent No. 6821724
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52.4%; 5
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Best Local Similarity 100.
Matches 11; Conservative
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Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 ATTCGTTGCTC 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 ATTCGTTGCTC 12
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; ORGANISM: Mus musculus
US-09-396-196G-14051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear
PCT-US93-12078-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 52.4%; Score 11; DB 5; Length 22; Best Local Similarity 100.0%; Pred. No. 2e+03; Matches 11; Conservative 0; Mismatches 0; Indels
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TELEPHONE NO: (512)499-4462
                                                                                                                                                                                                                                                                                       STATE: LEANS
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK/ASKII
COMPUTER: BIM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOOFWARE: WORDERFEECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12078
FILING DATE: UNKNOWN
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION:
PRIOR APPLICATION NUMBER: 07/992,900
FILING DATE: 16.12.92
ATTORNEY AGENT INFORMATION:
NAME: HODGINS, DANIEL S.
REGERENCE/POCKET NUMBER: UTFF046PCT
TELEPHONE: 512-320-720
TELEPHONE: 512-320-720
TELEPHONE: 512-320-720
TELEFRAX: 713-789-2676
TELEFRAX: 713-789-26
            CHEMICALLY-CONJUGATED IMMUNOTOXINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENT AND SPECIFIC CHEMICALLY-CONJUGATED IMMUNOTOXINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201 West 7th Street
Austin
TITLE OF INVENTION: CHEMICALLY-CONJUGATITLE OF INVENTION: IMMUNDENCE SINGUMES: 5 CORRESPONDENCE ADDRESS: ADDRESSE: ARNOLD, WHITE & DURKEE STREET: P.O. BOX 4433
CITY: HOUSTON
STATE: TEXAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOSEE: ARNOLD, WHITE & DURKEE TT: P.O. BOX 4433 HOUSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (512) 499-4523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application PC/TUS9312078 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US91-12078-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 ATTCGTTGCTC 12
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APPLICANT:
SYSTEM
APPLICANT:
SYSTEM
APPLICANT:
APPLICAN
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ADDRESSEE: ARNOLD, W
STREET: P.O. BOX 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
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ZIP: 77210
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Query Match 52.4%; Score 11; DB 4; Length 25; Best Local Similarity 100.0%; Pred. No. 2e+03; Matches 11; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
US-09-196-196G-66427/C

Sequence 66427, Application US/09396196G

Patent No. 6821724

GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE REFERENCE: 3101.1

CURRENT APPLICATION NUMBER: US/09/396,196G

CURRENT FILING DATE: 1999-09-15

PRIOR FILING DATE: 1998-09-15

NUMBER OF SEQ ID NOS: 127806

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 66427

LENGTH: 25

LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-36-196G-66426/C

Sequence 66426, Application US/09396196G

Patent No. 6821724

GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Mack
APPLICANT: Affwertix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.
CURRENT FILING DATE: 1999-09-15
PRIOR PLING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 64426
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 18111
LENGTH: 25
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US-09-396-196G-66426
                                                                                                                                                             TYPE: DNA ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: mus musculus
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Best Local Similarity
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US-09-306-196G-18110
iS-09-306-196G-18110
sequence 18110, Application US/09396196G
sequence 18110, Application US/09396196G
set to 18110, Application US/09396196G
set to 18110 S
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Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Mack
APPLICANT: David Mack
APPLICANT: David Mack
APPLICANT: APPLICANT: AI
                      APPLICANT: David Mack
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT PILING DATE: 1999-09-15
PRIOR PILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SEQTHARR: FastESEQ for Windows Version 4.0
SEQTHARR: 25
   APPLICANT: Michael Mittmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 52.4
Best Local Similarity 100.
Matches 11; Conservative
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Matches 11; Conservative
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US-09-396-196G-18110
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| Patent No. 6074851
| GENERAL INFORMATION:
| APPLICANT: Deibel Jr., M. R. |
| APPLICANT: Wilson, C. L. |
| TILLE OF INVENTION: Like Activity |
| NUMBER OF SEQUENCES: 45 |
| CORRESPONDENCE ADDRESS: |
| ADDRESSES: Pharmacia & Upjohn Company |
| STREET: 301 Henrietta Street
    52.4%; Score 11; DB 4; Length 25; 100.0%; Pred. No. 2e+03; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.4%; Score 11; DB 4; Length 25; 100.0%; Pred. No. 2e+03; tive 0; Mismatches 0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/848,810
FILING DATE:
                                                                                                                                                                                                  US-09-396-196G-66438/c

Sequence 66438, Application US/09396196G

Patent No. 6821724

GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE BEFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
CURRENT FILING DATE: 1998-09-15
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 66438
LERGTH: 25
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NAME: Wocton, Thomas A.
REGISTRATION NUMBER: 35,004
TELECOMMUNICATION:
TELEPHONE: 616-833-7914
Query Match
Best Local Similarity 100.
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100
Matches 11; Conservative
                                                                                  7 TTGCTCCGCTC 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
CORGANISM: mus musculus
US-09-396-196G-66438
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US-08-848-810-42/c
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STATE: M1
COUNTRY:
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; TELEFAX: 616-833-6897
; INFORMATION FOR SEQ ID NO: 42: SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; TYPE:
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Pseudomon

		c 21	11	52.4	22	2 A	AAQ68396	
	GenCore version 5.1.6	c 22	11	52.4	53	2 A	AAX80489	
	Copyright (c) 1993 - 2005 Compugen Ltd.	c 53	11	52.4	53	4	AAS59324	
		C 24	11	52.4	58	¥ 9	ABA90993	
		c 25	11	52.4	53	12	AD061037	
OM nucleic - nu	OM nucleic - nucleic search, using sw model	c 26	11	52.4	30	2 A	AAQ78253	
		27	11	52.4	30	3 A	AA50463	
Run on:	September 12, 2005, 14:04:18; Search time 174 Seconds	28	10	47.6	17	2 A	AAV96406	
•	(without alignments)	29	10	47.6	17	2 A	AAV96405	
	714.452 Million cell updates/sec	30	10	47.6	11	9 9	ACN01300	
		c 31	10	47.6	17	9 9	ACN12384	
Title:	US-10-721-693-2	c 35	10	47.6	17	9 9	ACN14271	
Perfect score:	21	33	10	47.6	17	9 9	ACN04597	
Seguence:	1 aattegttgeteegetettgg 21	Ċ 34	10	47.6	17	9 9	ACN14270	
		35	10	47.6	17	9 9	ACN03280	
Scoring table:	Scoring table: OLIGO_NUC	36	10	47.6	17	9 9	ACN04596	
	Gapop 60.0 , Gapext 60.0	c 37	10	47.6	17	9 9	ACN12383	
		38	10	47.6	11	9 9	ACN01301	
Searched:	4390206 segs, 2959870667 residues	39	10	47.6	11	9 9	ACN03279	
		ο 40	10	47.6	11	9 9	ACN09757	
Word size :	0	c 41	10	47.6	17	10	ADI49330	
		42	10	47.6	18	3	AAA52028	
Total number of	Total number of hits satisfying chosen parameters: 2557800	c 43	10	47.6	18	5 A	AS12190	
		44	10	47.6	18	۲ 9	AAD40983	
Minimum DB seq	length: 15	c 45	10	47.6	18	¥ 9	ABK29394	
Maximum DB seq length: 30	length: 30							
Post-processing	Post-processing: Listing first 45 summaries						ALIGNMENTS	တ

Aax80489 Human sec Aba99324 Human sec Aba9093 Biotinyla Aba9093 Biotinyla Aad78253 Primer to Aaa50463 Human zin Aav86405 Potato ci Aav86405 Potato ci Acn01300 WNV Hamme Acn1231 WNV Minus Acn14271 WNV Minus Acn4271 WNV Minus Acn6597 WNV Zinzy Acn659 WNV Zinzy Acn6598 WNV Zinzy Acn6598 WNV Zinzy Acn61381 WNV Minus Acn013101 WNV Hamme Acn01301 WNV Hamme Acn01301 WNV Hamme Acn01301 WNV Inozy Acn6577 WNV Minus Acn63779 WNV Minus

ALIGNMENTS

Aaa52028 Antisense Aas12190 Human Int Aad40983 Human PI3 Abk29394 Penicilli

neurodegenerative disorder, CNS; Parkinson's disease; Alzheimer's; Huntington's; spinocerebellar ataxia type 1; spinocerebellar ataxia type 3; SCA; Machado-Joseph disease; dentatorubral-pallidoluysian atrophy; DRPLA; siRNA; small interfering RNA; ss; human; ataxin 1. Antiense DNA 2 encoding an siRNA targeted to human ataxin 1 mRNA. ADP44614 standard; DNA; 21 BP. (first entry) 26-AUG-2004 ADP44614; RESULT 1 ADP44614

Homo sapiens.

WO2004047872-A2.

10-JUN-2004.

26-NOV-2003; 2003WO-US037650.

26-NOV-2002; 2002US-0429387P. 03-FEB-2003; 2003US-0444614P.

(MEDT) MEDTRONIC INC.

Kaemmerer WF;

WPI; 2004-441106/41.

New medical system comprising an intracranial access device, a mapping means, a small interfering RNA or vector encoding the RNA, and a delivery means, useful for treating a neurodegenerative disorder.

Claim 68; SEQ ID NO 4; 228pp; English.

The invention relates to a novel medical system for treating a beurodegenerative disorder comprising an intracranial access device, a mapping means for locating a predetermined location in the brain, a deliverable amount of a small interfering RNA (siRNA), or vector encoding

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geneseqn2003cs:* geneseqn2003ds:* geneseqn2004as:* geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES Description	4614 4612 Adp44614 Antiense 4613 Adp44612 Antiense 4611 Adp44611 Sense DNA 4611 Ada203368 PCR prime 427 Adx86972 Primer of Adx86972 Primer of Adx19405 Adx19400 Adx10400 Adx104000 Adx1040000 Adx10400000000000000000000000000000000000
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                 applications related to the CNS and may be useful for treating a neurodegenerative disorder, such as Parkinson's disease, Alzheimer's disease, Huntington's disease, spinocerebellar ataxia (SCA) types 1 and 3 (Machado-Joseph disease) or dentatorubral-pallidoluysian atrophy (DRPLA). The current sequence is that of the antisense DNA 2 encoding an siRNA targeted to human ataxin 1 mRNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New medical system comprising an intracranial access device, a mapping means, a small interfering RNA or vector encoding the RNA, and a delivery means, useful for treating a neurodegenerative disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a novel medical system for treating a neurodegenerative disorder comprising an intracranial access device, a mapping means for locating a predetermined location in the brain, a deliverable amount of a small interfering RNA (siRNA), or vector encoding the siRNA, and a delivery means. The system of the invention has applications related to the CNS and may be useful for treating a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neurodegenerative disorder, such as Parkinson's disease, Alzheimer's disease, Huntington's disease, spinocerebellar ataxia (SCA) types 1 and 3 (Machado-Joseph disease) or dentatorubral-pallidoluysian atrophy (DRPLA). The current sequence is that of the antisense DNA 1 encoding an siRNA targeted to human ataxin 1 mRNA of the invention.
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and a delivery means. The system of the invention has
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spinocerebellar ataxia type 3; SCN; Machado-Joseph disease;
dentatorubral-pallidoluyalan atrophy; DRPLA; siRNA;
small interfering RNA; ss; human; ataxin 1.
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100.0%; Pred. No.
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Pred. No. 0.0091;
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Pred. No.
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03-FEB-2003; 2003US-0444614P.
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ADP44611 standard; DNA; 21
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es 19; Conserv
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Chlamydia trachomatis.
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              Synthetic
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                                                                        encoding an siRNA targeted to human ataxin 1 mRNA
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spinocerebellar ataxia type 3; SCA; Machado-Joseph disease;
dentatorubral-pallidoluysian atrophy; DRPLA; siRNA;
small interfering RNA; ss; human; ataxin 1.
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Pred. No. 0.14;
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PCR primers AA201426-206209 were used to amplify open reading frames (ORFs) of the genome of Chlamydia trachomatis (see AA201425). These ORFs encode polypeptides (see AAX36754-X37949) which can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye diseases such as conventional trachoma, nonnendemic trachoma, paratrachoma, and inclusion epidymitis, cervicitis, salpingitis, perihepatitis, bartholinitis, pneumopachy in breast feeding infants; and veneral lymphogranulomatosis. The polypeptides of the invention may be of use in treating these
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                                                                                                                                                                                                                                                                                                                                                                                                       Genome sequence of Chlamydia trachomatis.
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                                                         97FR-00015041.
97FR-00016034.
98US-0107077P.
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98WO-IB001939
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The present invention describes the isolation of nucleic acid (I) that encodes a protein (II) having a signal peptide (SP), which comprises isolating RNA moleculas (III) that are associated with microsomes under conditions where (II) is at least partly translated. Also described are: (1) a library of (I) encoding (II) comprising SP; (2) (I) isolated by the above method; and (3) (II) encoded by (II. (I) and (II) are useful to the translated and (3) (II) encoded by (II. (I) and (II) are useful to the above method; and (3) (II) encoded by (II. (I) and (II) are useful in treatment of cancer. (I) are also used: as tissue and molecular weight markers; as chromosome tags; to detect possible genetic disorders; as hybridisation probes to identify related nucleic acid; as primers for DNA fingerprinting; to generate antibodies; and in interaction trap assays to identify gene encoding specific binding agents. (II) are useful in drug screening, for raising antibodies (e.g. for use as immunoassay reagents) and to induce an immune response. The method is more efficient and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolating nucleic acids encoding proteins comprising a signal peptide - by translating RNA and isolating translated RNA that is associated with microsomes, useful as therapeutic agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               reliable than the sequence trap system. It does not involve formation of
a fusion protein (rather natural proteins are selected) and (II) do not
have to be secreted. The present sequence represents a PCR primer which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 52.4%; Score 11; DB 2; Length 20; Best Local Similarity 100.0%; Pred. No. 7.8e+03; Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Secreted protein; microsome; signal peptide; PCR primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20 BP; 7 A; 3 C; 7 G; 3 T; 0 U; 0 Other;
52.4%; Score 11; DB 12; 100.0%; Pred. No. 7.8e+03; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          is used in an example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                            Neurogenin protein PCR forward primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Page 34; 45pp; English
                                                                                                                                                                                                                                                   Query Match 52.4
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                        8 TGCTCCGCTCT 18
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                                                                                                                                                           15 TGCTCCGCTCT
                                                                                                                                                                                                                                      RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a purified secreted Chlamydia protein, which is identified by its expression by a Gram-negative bacterial strain and secretion by the type III secretion pathway of the bacterium. This can be used to diagnose, treat and vaccinate against Chlamydia infection in a patient, which may contribute to atherosclerosis or a sexually transmitted disease. The present sequence is a PCR primer used to produce fusion constructs in the exemplification of the invention
                                                                                                                                                                                                         Novel purified secreted Chlamydia polypeptide which is identified by its secretion in a Gram-negative bacterial strain containing a type III secretion pathway, useful for treating Chlamydia infections in humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to a polynucleotide isolated from a human gene and is useful for detecting a single nucleotide polymorphism in a human gene or for diagnosing of disease. The invention enables the detection of a single nucleotide polymorphism in a human gene. The present sequence represents a primer of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel polynucleotide useful for PCR amplification along with two DNA fragment from another set of sequences, or for detecting single nucleotide polymorphism in human gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57.1%; Score 12; DB 6; Length 30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human; single nucleotide polymorphism; SNP; ss; primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 30 BP; 6 A; 6 C; 8 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 1.9e+03;
  (INSP ) INST PASTEUR.
(CNRS ) CNRS CENT NAT RECH SCI.
(INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Pred. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
                                                                                                        Dautry-Varsat A;
                                                                                                                                                                                                                                                                                                                 Example 1; Page 28; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Primer of the invention #2692.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-MAR-2002; 2002JP-00064373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADK96972 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AATTCGTTGCTC 12
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                                                                                                        Parsot C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-093977/10.
                                                                                                                                                           WPI; 2002-583484/62
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06-MAY-2004

ADK96972;

RESULT 7 ADK96972/c

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Query Match

Matches

16-SEP-2003

Synthetic

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Sequence 19 BP; 4 A; 4 C; 8 G; 3 T; 0 U; 0 Other;

involve formation of ted) and (II) do not

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The invention relates to Xenopus lasvis Zic3 protein (AAY69524). Zic3 contains a zinc finger motif, and induces the formation of neurons. The CDNA was obtained from embryonic Xenopus nerve poly(A+) RNA. Zic3, and nucleotides encoding it, are useful as diagnostic tools for neurological diseases, and for the treatment of Alzheimer's disease. Sequences are expressed with Zic3 in various Xenopus cell types in an expressed with Zic3 in various Xenopus cell types in an
Neurogenin, Zic3; zinc finger; neuroregeneration; neurological disease; diagnosis; Alzheimer's disease; expression pattern; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ITS; internal transcribed spacer region; Mycobacterium fortuitum; Mycobacterium chelonae; Mycobacterium abscessus; Mycobacterium vaccae; Mycobacterium flavescens; Mycobacterium asiaticum; tuberculosis; Mycobacterium asiaticum; tuberculosis; Mycobacterium porcinum; Mycobacterium acapulcensis; identification; Mycobacterium diernhoferi; PCR primer; probe; detection; ss.
                                                                                                                                                                                                                                                                                                                              formation-inducing gene - useful as a diagnostic agent for diseases, and for treating Alzheimer disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oligonucleotide for detection of Mycobacterium porcinum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52.4%; Score 11; DB 3; Le 100.0%; Pred. No. 7.8e+03; iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence 20 BP; 7 A; 3 C; 7 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Page 14; 30pp; Japanese
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99KR-00019632.
99KR-00019633.
99KR-00019634.
2000KR-00018189.
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                                                                                                                                                                             98JP-00121456
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                                                                                                                                                                                                                                                      (RIKA ) RIKAGAKU KENKYUSHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAF23328 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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Best Local Similarity 100.
Matches 11, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 CTCCGCTCTTG 1
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                                                                                                                                                                                                                                                                                             WPI; 2000-101694/09
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                                                                                                 JP11341985-A.
                                                                                                                                                                                                                  31-MAR-1998;
                                                                                                                                                                             30-APR-1998;
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29-MAY-1999;
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29-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                    nerve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCR primers AAZ01426-Z06209 were used to amplify open reading frames core polypeptides (see AAX16754-Y37949) which can be used as vaccines against Chlamydia trachomatis. (see AAX16755. These ORFs against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye diseases such as conventional trachom, nonendemic trachoma, paratrachoma, and inclusion epidymitis; genital diseases such as nongonococcal uretritis, previcitis, expiratis, perimpatitis, perimpatitis, paratracholinitis; penumopathy in breast feeding infants; and venereal lymphogranulomatosis.
                                                                                                                                                                                                                Vaccine, eye disease, conventional trachoma, nonendemic trachoma, paratrachoma, inclusion conjunctivitis, genital disease, perihepatitis, nongonococcal uretritis, epidymitis, cervicitis, salpingitis, PCR primer, bartholinitis, pneumopathy, venereal lymphogranulomatosis, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                         primer used to amplify an ORF of Chlamydia trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52.4%; Score 11; DB 2; Length 20; 100.0%; Pred. No. 7.8e+03; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome sequence of Chlamydia trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure, Page 1675; 1755pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAZ55953 standard; cDNA; 20 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97FR-00015041.
97FR-00016034.
98US-0107077P.
                                                         AAZ04279 standard; DNA; 20 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                      98WO-IB001939
                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                             Synthetic.
Chlamydia trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCGTTGCTCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-NCV-1997;
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                                                                                                                                    07-OCT-1999
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04-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                             10-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Griffais R;
                                                                                               AAZ04279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15
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RESULT 10

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AAZSSSSS 1D AAZS XX AAZS AC AAZS XX 10-A XX 10-A XX XX

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numerical gene expression values between samples of genes. The method comprises amplifying CDNA in the presence of a competitive template mixture and primer pairs everal genes and then amplifying aliquots of the PCR products using a primer pair specific for each gene. The method of amplification is by multiplex standardised reverse transcriptuse-polymerse chain reaction (StaRT-PCR). High density oligonucleotide or CDNA arrays are useful for the assessment of gene expression in small biological samples such as fine needle aspirate blopsies, and laser captured microdissected materials. The method allows for the standardised measurement of hundreds of genes from the same sample, which in prior art, could only be assessed for one gene. The present sequence represents a multiplex StaRT-PCR primer which can be used in the method of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; antisense; lung dysfunction; nasal airway dysfunction; antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiinflammic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.
                                                                           Direct comparison of numerical gene expression values between samples of genes comprises using multiplex standardized reverse transcription-polymerase chain reaction.
                                                                                                                                                                                                                                            The present invention relates to a method for the direct comparison of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
Tang L, Shahabuddin S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52.4%; Score 11; DB 10; Length 20; 100.0%; Pred. No. 7.8e+03; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20 BP; 1 A; 8 C; 4 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                          Example 1; SEQ ID NO 143; 59pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABZ97696 standard; DNA; 20 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-OCT-2003 (first entry)
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                           WPI; 2003-811730/76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200285308-A2.
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Miller S,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M. vaccae, M. flavescens, M. salaticum, M. porcinum, M. acapulcensis, M. diernhoferi genes were leantified. The Oligonucleotides derived from these sequences were used to develop PCR primers and hybridisation probes for detection and identification of Mycobacterium. ITS has a more polymorphic region than 165 rRNA and also has a conserved region. It is therefore highly effective as a target DNA for distinction of genotype. The Oligonucleotide probes, attached to solid substrate, hybridise only with nucleotide sequences in ITS of specific mycobacteria, and thus they can detect and identify the specific mycobacteria sensitively. The Oligonucleotides can also detect and identify the specific mycobacteria by PCR amplification. Using the Oligonucleotide primers or probes made from ITS of mycobacteria, it is possible to detect mycobacteria distinguish tuberculosis (TB) complex from non-tuberculosis mycobacteria (NTM), and to identify mycobacteria species accurately and effectively
                                                                                                                                                                                                                      region of
                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is an oligonucleotide developed using a Mycobacterium ITS (internal transcribed spacer region) nucleotide sequence. ITS DNA sequences from M. fortuitum, M. chelonae, M. abscessus,
                                                                                                                                                                                                           Novel oligonucleotide sequences of internal transcribing spacer region non-tuberculosis mycobacteria (NTM) used as probes or primers for detecting and identifying mycobacteria and distinguish TB complex from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human gene expression analysis multiplex StaRT-PCR primer #143.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52.4%; Score 11; DB 4; Length 20; 100.0%; Pred. No. 7.8e+03;
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                                                                                                                                                                                                                                                                                                                                                      Claim 34; Page 78; 89pp; English.
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                                                                                                               Jang HJ;
SJ HIGHTECH CO LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTTGCTCCGCT
                                                                                                                                                              WPI; 2001-061527/07
                           KIM C M.
PARK H K.
                                                                                                            Park HK,
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(PARK/)
                                                                                                            Kim CM,
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The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the intitation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition may have a use in antisense therapy. The composition may have a use in antisense year the respiratory, lung or therapeutic respiratory effect of an entiting managency steroid in a subject, for reducing levels of for enhancing the prophylactic or therapeutic respiratory effect of antiinflammatory steroid in a subject, for reducing levels of adenosine receptor, producing bronchodilation, increasing levels of adenosine creeptor, producing bronchodilation, increasing levels of ubiquinone or lung suffactant in a subject, a respiratory disease or condition. The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 12938; 872pp; English.
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ubiquinone.
\mathbb{E} \times \mathbb{E} \times
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Sequence 20 BP; 3 A; 7 C; 3 G; 7 T; 0 U; 0 Other;

Gaps ö 52.4%; Score 11; DB 10; Length 20; 100.0%; Pred. No. 7.8e+03; ive 0; Mismatches 0; Indels 52.4%; Query Match
Best Local Similarity 100.

ઠ 셤 RESULT 14

ABZ97695 standard; DNA; 20 BP. ABZ97695

17-OCT-2003 (first entry) ABZ97695;

Human CCR3 oligonucleotide sequence.

Human; antisense; lung dysfunction; nasal airway dysfunction; antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.

Homo sapiens,

WO200285308-A2.

31-OCT-2002.

23-APR-2002; 2002WO-US013135.

24-APR-2001; 2001US-0286137P.

(EPIG-) EPIGENESIS PHARM INC Nyce JW,

Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D; Tang L, Shahabuddin S; WPI; 2003-229219/22. Miller S,

Pharmaceutical composition for treating ailments associated with impaired

respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonuclectide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an entinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an artiinflammatory steroid in a subject, for reducing levels of adenosine or receptor, producing bronchodilation, increasing levels of adenosine receptor, producing bronchodilation, increasing levels of usigninone or lung surfactant in a subject's tissue, or treating bronchoconstriction, ung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO Disclosure; SEQ ID NO 12937; 872pp; English. at ftp.wipo.int/pub/published_pct_sequences ubiquinone

Sequence 20 BP; 3 A; 7 C; 5 G; 5 T; 0 U; 0 Other;

Gaps ; 0 Length 20; Indels 52.4%; Score 11; DB 10; I 100.0%; Pred. No. 7.8e+03; ive 0; Mismatches 0; Query Match 52.4 Best Local Similarity 100. Matches 11, Conservative

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RESULT 15 ABD30726

ABD30726 standard; DNA; 20 BP.

ABD30726;

29-JUL-2004 (first entry)

Human CCR3-derived oligonucleotide SEQ ID 12937.

Human; antisense; bronchoconstriction; allergy; hyposecretion; pain; respiratory tract inflammation; adenosine sensitivity; lung; cancer; surfactant depletion; antiallergic; antinflammatory; antiasthmatic; analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis; beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction; respiratory distress syndrome; allergic rhinitis; pulmonary hypertension; emphysema; chronic obstructive pulmonary disease; cancer; bronchitis; pulmonary transplantation rejection; 88; primer.

Homo sapiens.

WO200285309-A2

31-0CT-2002.

23-APR-2002; 2002WO-US013143.

24-APR-2001; 2001US-0286036P.

(EPIG-). EPIGENESIS PHARM INC.

Katz E, Pabalan J, Aguilar D; Li Y, Sandrasagra A, K, Tang L, Shahabuddin S; Nyce JW, Miller S,

WPI; 2003-093058/08.

Pharmaceutical composition for treating asthma, has antisense

oligonucleotide containing less percentage of adenosine, targeted to nucleic acids associated with lung airway or lung dysfunction, and bronchodilating agent.

Claim 15; SEQ ID NO 12937; 763pp; English.

The invention also describes a kit, that comprises: (a) a delivery device, in separate containers, (b) the oligonucleotides, (c) device, in separate containers, (b) the oligonucleotides, (c) device, in separate containers, (b) the oligonucleotides, (c) constrained a carrier and for use of the kit. The composition of the invention has antiallergic, antiinflammatory, antiasthmatic, analgesic, hypotensive, immunosuppressive and cytostatic activity, is a consosition comprises oligo or malignant disease. The administered composition comprises oligo and is administered to reduce the production comprises oligo and is administered to reduce the production or availability, or to increase the degradation of the target mRNA or to reduce the amount of target polypeptide present in the lungs. The cultinammation, and/or bronchoconstriction and/or lung to inflammation, allergies and/or surfactant hypoproduction are associated with a disease or condition such as pulmonary vasoconstriction, and seems or condition such as pulmonary disease, pulmonary conting manualion, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary transplantation rejection, pulmonary infections, bronchitis or cancer.

The reduced adenosine content of the anti-sense oligos corresponding to the oligonucleotides into products that free adenosine into the system ceg., lung, brain, heart, kidney, etc, tissue environment and thereby, to prevent any unwanted effects due to it This invention describes a novel composition (a) a first active agent, comprising oligonucleotides, effective for alleviating bronchoconstriction, respiratory fract inflammation, allergies and reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors, surfactant depletion or hyposecretion, when administered to a mammal. The oligonucleotides are derived from a gene encoding or resplating expression of a target polypeptide associated with lung airway or lung dysfunction or cancer and can be anti-sense to the corresponding mRNA.

Sequence 20 BP; 3 A; 7 C; 5 G; 5 T; 0 U; 0 Other;

Gaps ; 0 Query Match 52.4%; Score 11; DB 11; Length 20; Best Local Similarity 100.0%; Pred. No. 7.8e+03; Matches 11; Conservative 0; Mismatches 0; Indels

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Search completed: September 12, 2005, 17:04:31 Job time : 175 secs

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September 12, 2005, 14:04:18; Search time 174 Seconds (without alignments) 714.452 Million cell updates/sec
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4390206 segs, 2959870667 residues 1 aaccaagagcggagcaacgaa 21 OLIGO NUC Gapop 60.0 , Gapext 60.0 0 Scoring table: score: Word size : Title: Perfect so Sequence: Searched:

Total number of hits satisfying chosen parameters: Minimum DB seq length: 15 Maximum DB seq length: 30

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summaries Post-processing: Listing first 45

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Adp44613 Sense DNA	Adp44611 Sense DNA	Adp44614 Antiense	Adp44612 Antiense	Aci35330 Human mic	Adk96972 Primer of	Aax19405 Neurogeni	Aaz03368 PCR prime	Aaz04279 PCR prime	Aaz55953 Xenopus l	Aaf23328 Oligonucl	Add56623 Human gen	Abz97696 Human CCR	Abz97695 Human CCR	Abd30726 Human CCR	Abd30727 Human CCR	Adj59552 Oligonucl	Adj59553 Oligonucl	Ado45043 Human oli	Ado45042 Human oli
SUMMARIES	OI.	ADP44613	ADP44611	ADP44614	ADP44612	ACI35330	ADK96972	AAX19405	AAZ03368	AAZ04279	AAZ55953	AAF23328	ADD56623	AB297696	ABZ97695	ABD30726	ABD30727	ADJ59552	ADJ59553	ADO45043	AD045042
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	A Query Match	100.0	100.0	90.5	90.5	57.1	52.4	52.4	52.4	52.4	52.4	52.4	52.4	52.4	52.4	52.4	52.4	52.4	52.4	52.4	52.4
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21 11 52.4 24 111 52.4 25 11 52.4 26 11 52.4 27 11 52.4 29 11 52.4 31 11 52.4 47.6 31 10 47.6 33 10 47.6 34 10 47.6 36 10 47.6 37 10 47.6 41 10 47.6 41 10 47.6 42 10 47.6 43 10 47.6 44 10 47.6 45 10 47.6 46 10 47.6 47 6 48 10 47.6 49 10 47.6 49 10 47.6 41 10 47.6 42 10 47.6 43 10 47.6 44 10 47.6 45 10 47.6 46 10 47.6 47 6 48 10 47.6 48 10 47.6 49 10 47.6 40 10 47.6 41 10 47.6 42 10 47.6 43 10 47.6	
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ALIGNMENTS

neurodegenerative disorder, CNS; Parkinson's disease; Alzheimer's; Huntington's; spinocerebellar ataxia type 1; spinocerebellar ataxia type 3; SCA; Machado-Joseph disease; dentatorubral-pallidolluysian atrophy; DRPLA; siRNA; small interfering RNA; 88; human; ataxin 1. Sense DNA 2 encoding an siRNA targeted to human ataxin 1 mRNA. ADP44613 standard; DNA; 21 BP. (first entry) 26-AUG-2004 ADP44613; RESULT 1 ADP44613

26-NOV-2003; 2003WO-US037650. WO2004047872-A2. Homo sapiens. 10-JUN-2004

26-NOV-2002; 2002US-0429387P. 03-FEB-2003; 2003US-0444614P. (MEDT) MEDTRONIC INC. WPI; 2004-441106/41. Kaemmerer WF;

New medical system comprising an intracranial access device, a mapping means, a small interfering RNA or vector encoding the RNA, and a delivery means, useful for treating a neurodegenerative disorder.

Claim 68; SEQ ID NO 3; 228pp; English.

The invention relates to a novel medical system for treating a neurodegenerative disorder comprising an intracranial access device, a mapping means for locating a predetermined location in the brain, a deliverable amount of a small interfering RNA (siRNA), or vector encoding

Pred. No. 0.013;

100.08;

Best Local Similarity

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                                 applications related to the CNS and may be useful for treating a neurodegenerative disorder, such as Parkinson's disease, Alzheimer's disease, Huntington's disease, spinocerebellar ataxia (SCA) types 1 and 3 (Machado-Joseph disease) or dentatorubral-pallidoluysian atrophy (DRPLA). The current sequence is that of the sense DNA 2 encoding an siRNA targeted to human ataxin 1 mRNA of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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and a delivery means. The system of the invention has
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA 1 encoding an siRNA targeted to human ataxin 1 mRNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-441106/41.
                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-AUG-2004
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   BiRNA,
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                                                                                                                                                                                                                                                                                                                                                          Query Match
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ADP44611
ADP4611
ADP4
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DB 12; Length 21;

100.0%; Score 21;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a novel medical system for treating a neurodegenerative disorder comprising an intracranial access device, a mapping means for locating a predetermined location in the brain, a deliverable amount of a small interfering RNA (siRNA), or vector encoding the siRNA, and a delivery means. The system of the invention has applications related to the CNS and may be useful for treating a neurodegenerative disorder, such as Parkinson's disease, Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New medical system comprising an intracranial access device, a mapping means, a small interfering RNA or vector encoding the RNA, and a delivery means, useful for treating a neurodegenerative disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disease, Huntington's disease, spinocerebellar ataxia (SCA) types 1 and (Machado-Joseph disease) or dentatorubral-pallidoluysian atrophy (DRPLA) The current sequence is that of the antisense DNA 2 encoding an SiRNA targeted to human ataxin 1 mRNA of the invention.
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                       Antiense DNA 2 encoding an siRNA targeted to human ataxin 1 mRNA.
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                                                                                                                                                                                                                                                                                      Huntington's; spinocerebellar ataxia type 1;
spinocerebellar ataxia type 3; SCA; Machado-Joseph disease;
dentatorubral-pallidoluysian atrophy; DRPLA; siRNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 12; Length 21; 0.18;
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Indels
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                                                                                                                                                                                                                                                                                                                                      small interfering RNA; ss; human; ataxin 1.
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 Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 68; SEQ ID NO 4; 228pp; English
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100.0%; Pred
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                                                             1 AACCAAGAGCGGAGCAACGAA
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                               1 AACCAAGAGCGGAGCAACGAA
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Best Local Similarity
Local Similarity
Local 19;
Conservative
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                                                                                                                                           ADP44614 standard; DNA; 21
                                                                                                                                                                                                         (first entry)
   21; Conservative
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   Matches
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                                                                                                              RESULT 3
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15-MAR-2002; 2002US-00098263 16-MAR-2001; 2001US-0276759P

US2003104410-A1

05-JUN-2003

Homo sapiens.

(AFFY-) AFFYMETRIX INC

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The invention relates to a novel medical system for treating a neurodegenerative disorder comprising an intracranial access device, a mapping means for locating a predetermined location in the brain, a deliverable amount of a small interfering RNA (siRNA), or vector encoding applications related to the CNS and may be useful for treating a neurodegenerative disorder, such as Parkinson's disease, Alzheimer's disease, Huntington's disease, spinocerebellar ataxia (SCA) types 1 and 3 (Machado-Joseph disease) or dencatorubral-pallidoluysian atrophy (DRPLA). The current sequence is that of the antisense DNA 1 encoding an siRNA targeted to human ataxin 1 mRNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New medical system comprising an intracranial access device, a mapping means, a small interfering RNA or vector encoding the RNA, and a delivery means, useful for treating a neurodegenerative disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST; 88; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human; cross-species comparison.
                                                                                                                  neurodegenerative disorder; CNS; Parkinson's disease; Alzheimer's;
Huntington's; spinocerebellar ataxia type 1;
spinocerebellar ataxia type 3; SCA; Machado-Joseph disease;
dentatorubral-pallidoluysian atrophy; DRPLA; siRNA;
small interfering RNA; ss; human, ataxin 1.
                                                                                   Antiense DNA 1 encoding an siRNA targeted to human ataxin 1 mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90.5%; Score 19; DB 12; Length 21; 100.0%; Pred. No. 0.18; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human microarray DNA oligonucleotide SEQ ID NO 35321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 21 BP; 2 A; 6 C; 5 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 68; SEQ ID NO 2; 228pp; English
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                                                                                                                                                                                                                                                                                                                                                                 26-NOV-2002; 2002US-0429387P.
03-FEB-2003; 2003US-0444614P.
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                                                26-AUG-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                     (MEDT ) MEDTRONIC INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kaemmerer WF;
                                                                                                                                                                                                                            Homo sapiens
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                  ADP44612;
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AC135330/c
1D AC13533
XX
AC AC1353
XX
DT 13-OCT-
XX
XX
XX
KW EST; 86
KW Genetic
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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch.

Calso disclosed is a method of gene expression analysis. The array is used in analysis of genetic variation or in hybridisation to a DNA library, compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises of at least one target sequence. The method of analysis comprises of at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, cor family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid further comprises a tag sequence. The array of nucleic acid further comprises a tag sequence or specific containing the 5' termini of mRNA molecules by comparisons of any gene, in mapping the 5' termini of mRNA molecules by containing sequents of DNA that have been containing sequence presented is one of the mucleic acid probes incorporated in the microarray. Note: The sequence and probes incorporated in the microarray. Note: The sequence can also be obtained in electronic format directly from USPTO at sequence.html
                                                                                                                                                                                                                                                                                                                New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 25 BP; 2 A; 5 C; 6 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 35321; 9pp; English
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Bost Local Similarity 100.00
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임
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28-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolating nucleic acids encoding proteins comprising a signal peptide - by translating RNA and isolating translated RNA that is associated with microsomes, useful as therapeutic agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     a human
                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a polynucleotide isolated from a human gene and is useful for detecting a single nucleotide polymorphism in a human gene or for diagnosing of disease. The invention enables the detection of a single nucleotide polymorphism in a human gene. The present sequence represents a primer of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                             Novel polynucleotide useful for PCR amplification along with two DNA
                                                                                                                                                                                                                                                                                                       from another set of sequences, or for detecting single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 19 BP; 4 A; 4 C; 8 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; SEQ ID NO 6001; 2627pp; Japanese.
                                                                                                                                                                  (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
                                                                                                                                                                                                                                                                                                                                       nucleotide polymorphism in human gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neurogenin protein PCR forward primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Page 34; 45pp; English
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                                                    08-MAR-2002; 2002JP-00064373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGAGCGGAGCA
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16-SEP-2003
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AX19405

AX19405

AX19405

AX2 AAX1

XX AX2

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therapeutically, typically (II) are cell growth factors such as cytokines, interleukins, colony-forming factors, possibly useful in treatment of cancer. (I) are also used: as tissue and molecular weight markers; as chromosome tags; to detect possible genetic disorders; as hybridisation probes to identify related nucleic acid; as primers for DNA fingerprinting; to generate antibodies; and in interaction trap assays to identify gene encoding specific binding agents. (II) are useful in drug screening, for raising antibodies (e.g. for use as immunoassay reagents) and to induce an immune response. The method is more efficient and reliable than the sequence trap system. It does not involve formation of a fusion protein (rather natural proteins are selected) and (II) do not have to be secreted. The present sequence represents a PCR primer which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCR primers AAZ01426-Z06209 were used to amplify open reading frames (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs encode polypeptides (see AAX36754-Y37949) which can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye diseases such as conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion conjunctivitis; genital diseases such as nongonococcal uretritis, epidymitis, cervicitis, aalpingitis, perihepatitis, bartholinitis; pneumopathy in breast feeding infants; and venereal lymphogranulomatosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vaccine; eye disease; conventional trachoma; nonendemic trachoma; paratrachoma; inclusion conjunctivitis; genital disease; perihapatitis; nongonococcal uretritis; epidymitis; cervicitis; salpingitis; PCR primer; bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCR primer used to amplify an ORF of Chlamydia trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                         52.4%; Score 11; DB 2; Length 20; 100.0%; Pred. No. 8.3e+03; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                            Sequence 20 BP; 7 A; 3 C; 7 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                               is used in an example from the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 1601; 1755pp; English.
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97FR-00016034.
98US-0107077P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAZ03368 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                         11; Conservative
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Best Local Similarity
Matches 11; Conserv
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BP.

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Neurogenin, Zic3; zinc finger; neuroregeneration; neurological dise
diagnosis; Alzheimer's disease; expression pattern; PCR primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                             formation-inducing gene - useful as a diagnostic agent for
                                                                                                                                                               Xenopus laevis neurogenin sense PCR primer, SEQ ID NO:31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            diseases, and for treating Alzheimer disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 2; Page 14; 30pp; Japanese.
                                                                                                                                                                                                                                                                                                                          98JP-00121456.
                                                                       AAZSS953 standard; cDNA; 20
                                                                                                                                                                                                                                                                                                                                                                                   (RIKA ) RIKAGAKU KENKYUSHO.
                                                                                                                                 (first entry)
 5 CGGAGCAACGA 15
                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-101694/09
                                                                                                                                                                                                                                     Xenopus laevis.
                                                                                                                                                                                                                                                                  JP11341985-A.
                                                                                                                                                                                                                                                                                                                          30-APR-1998;
                                                                                                                                                                                                                                                                                                                                                      31-MAR-1998;
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                                                                                                    AAZ55953;
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                                                                                                                                                                                                                                                                                                                                                    Vaccine, eye disease; conventional trachoma; nonendemic trachoma; paratrachoma; inclusion conjunctivits; genital disease; perihepatitis; nongonococcal uretritis; epidymitis; cervicitis; salpingitis; PCR primer; bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCR primers AAZ01426-Z06209 were used to amplify open reading frames (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs encode polypeptides (see AAY36754-Y37949) which can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye diseases such as conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion conventional trachom inclusion epidymitis; genital diseases such as nongonococcal uretritis, epidymitis, cervicitis, salpingitis, perihepatitis, bartholinitis; penemopathy in breast feeding infants; and venereal lymphogranulomatosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oneumopathy in breast feeding infants; and venereal lymphogranulomatosis. The polypeptides of the invention may be of use in treating these
                                                                                                   Gaps
The polypeptides of the invention may be of use in treating these
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                                                                                                                                                                                                                                                                                                                       PCR primer used to amplify an ORF of Chlamydia trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52.4%; Score 11; DB 2; Length 20; 100.0%; Pred. No. 8.3e+03; ive 0; Mismatches 0; Indels
                                                                    52.4%; Score 11; DB 2; Length 20; 100.0%; Pred. No. 8.3e+03; Pred. No. 8.3e+03; Indels cive 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;
                                         Sequence 20 BP; 8 A; 4 C; 6 G; 2 T; 0 U; 0 Other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome sequence of Chlamydia trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 1675; 1755pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97FR-00015041.
97FR-00016034.
98US-0107077P.
                                                                                                                                                                                                                                   AAZ04279 standard; DNA; 20 BP
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                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                   11; Conservative
                                                                                                                                               GGAGCAACGAA 12
                                                                                                                              11 GGAGCAACGAA 21
                                                                                                                                                                                                                                                                                                                                                                                                                                            Chlamydia trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-371125/31.
                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GEST ) GENSET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-NOV-1998;
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17-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                AAZ04279;
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                diseases
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                                                                                                   Matches
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AAZ04279
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The invention relates to Xenopus laevis Zic3 protein (AAY69524). Zic3 contains a zinc finger motif, and induces the formation of neurons. The CDNA was obtained from embryonic Xenopus nerve poly(A+) RNA. Zic3, and nucleotides encoding it, are useful as diagnostic tools for neurological diseases, and for the treatment of Alzheimer's disease. Sequences are expressed with Zic3 in various Xenopus cell types in an expressed with Zic3 in various Xenopus cell types in an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ITS; internal transcribed spacer region; Mycobacterium fortuitum;
                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                               52.4%; Score 11; DB 3; Length 20; 100.0%; Pred. No. 8.3e+03; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oligonucleotide for detection of Mycobacterium porcinum.
                                                                                                                                                                             Sequence 20 BP; 7 A; 3 C; 7 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                               AAF23328 standard; DNA; 20 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                       11; Conservative
                                                                                                                                                                                                                                                                                             4 CAAGAGCGGAG 14
                                                                                                                                                                                                                                                                                                                   1 CAAGAGCGGAG 11
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                                                                                                                                                                                                                                 Best Local Similarity
Matches 11; Conserv
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Gaps

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11; Conservative

Best Local Similarity Matches 11; Conservat

Query Match

10 CGGAGCAACGA 20

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The present invention relates to a method for the direct comparison of numerical gene expression values between samples of genes. The method compilitying cDNA in the presence of a competitive template comparises amplifying cDNA in the presence of a competitive template mixture and primer pairs for several genes and then amplifying aliquots of the PCR products using a primer pair specific for each gene. The method of amplification is by multiplex standardised reverse method of amplification is by multiplex standardised reverse cligonucleotide or cDNA arrays are used to measure PCR products following quantitative StaRT-PCR. The method is useful for the assessment of gene expression in small biological samples such as fine needle aspirate biopsies, and laser captured microdissected materials. The method allows for the standardised measurement of hundreds of genes from the same for the standardised measurement of hundreds of genes from the same present sequence represents a multiplex StaRT-PCR primer which can be used in the method of the present invention.
                                                                                                                                                                                                                                                                                                                                                                        Direct comparison of numerical gene expression values between samples of genes comprises using multiplex standardized reverse transcription-polymerase chain reaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; antisense; lung dysfunction, nasal airway dysfunction; antinflammatory steroid; ubiquinone; antinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52.4%; Score 11; DB 10; Length 20; 100.0%; Pred. No. 8.3e+03; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20 BP; 1 A; 8 C; 4 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; SEQ ID NO 143; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human CCR3 oligonucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-MAR-2002; 2002US-00109349
                                                                                                                                                                28-MAR-2002; 2002US-00109349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                     Crawford EL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 GGAGCAACGAA 21
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                                                                                                                                                                                                                                                                                                                                  WPI; 2003-811730/76.
                                                                                                                                                                                                               (WILL/) WILLEY J C. (CRAW/) CRAWFORD E
                    US2003186246-A1
                                                                   02-OCT-2003
                                                                                                                                                                                                                                                                                     Willey JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is an oligonucleotide developed using a Mycobacterium ITS (internal transcribed spacer region) nucleotide sequence. ITS DNA sequences from M. fortuitum, M. chelonae, M. abscessus, M. vaccae, M. flavescens, M. asiaticum, M. porcinum, M. acapulcensis, M. vaccae, M. ilavescens, M. asiaticum, M. porcinum, M. acapulcensis, M. chiese sequences were identified. The oligonucleotides derived from these sequences were used to develop PCR primers and hybridisation probes for detection and identification of Mycobacterium. ITS has a more polymorphic region than 16S rRNA and also has a conserved region. It is therefore highly effective as a target DNA for distinction of genotype. The oligonucleotide probes, attached to solid substrate, hybridise only with nucleotide sequences in ITS of specific mycobacteria, and thus they can detect and identify the specific mycobacteria, and thus they coligonucleotides can also detect and identify the specific mycobacteria by PCR amplification. Using the oligonuclectide primers or probes made from ITS of mycobacteria, it is possible to detect mycobacteria distinguish tuberculosis (TR) complex from non-tuberculosis mycobacteria distinguish tuberculosis (TR) complex from non-tuberculosis mycobacteria (NTM), and to identify mycobacteria species accurately and effectively
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel oligonucleotide sequences of internal transcribing spacer region of non-tuberculosis mycobacteria (NTM) used as probes or primers for detecting and identifying mycobacteria and distinguish TB complex from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human gene expression analysis multiplex StaRT-PCR primer #143.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.4%; Score 11; DB 4; Length 20; 100.0%; Pred. No. 8.3e+03;
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                                                                                                                                                             99KR-00019632.
99KR-00019633.
99KR-00019634.
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                                                                                          16-MAY-2000; 2000WO-KR000477
                                                                                                                                         99KR-00019631
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                                                                                                                                                                                                                                                                                                                                                                                                           Jang HJ;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                        Kim CM, Park HK,
                                                                                                                                                                                                                                                                                                                                                           (PARK/) PARK H K.
WO200073436-A1
                                                                                                                                                                29-MAY-1999;
29-MAY-1999;
29-MAY-1999;
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11D ADD566:
XX AC ADD566:
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XX BE Human g
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XX Homo scall 1
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NAMES OF COLOR COL

Matches

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Gaps

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first active agent comprising an oligomortocide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nuclecides of junctions of genee encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiliflammatory steroid and ubiquinone. A composition of the invention has antiliflammatory antiallargic, antiathmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antistanse gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antistand sensitivity to adenosine, reducing sensitivity to adenosine, reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of adenosine receptor, producing allergies, or a respiratory disease or condition, lung inflammation, lung allergies, or a respiratory disease or condition.

Specification, but was obtained in electronic format directly from WIPO are initial or an anti-printed and allergies.
                                                                                                                                                                                                                                                     Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a novel pharmaceutical composition, which has a
                                                                                                                            Pabalan J, Aguilar D;
                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 12938; 872pp; English.
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                                                                                                                            Katz E,
                                                                                                                         Li Y, Sandrasagra A, K
Tang L, Shahabuddin S;
                     24-APR-2001; 2001US-0286137P.
                                                                      (EPIG-) EPIGENESIS PHARM INC.
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                                                                                                                            Nyce JW,
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Sequence 20 BP; 3 A; 7 C; 3 G; 7 T; 0 U; 0 Other;

Gaps ö 52.4%; Score 11; DB 10; Length 20; 100.0%; Pred. No. 8.3e+03; ive 0; Mismatches 0; Indels Ouery Match Best Local Similarity 100. Matches 11; Conservative 7 GAGCGGAGCAA 17 ઠ

11 GAGCGGAGCAA 1

ABZ97695 standard; DNA; 20 BP RESULT 14

(first entry) 17-OCT-2003 ABZ97695;

Human CCR3 oligonucleotide sequence.

Human; antisense; lung dysfunction; nasal airway dysfunction; antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchodonstriction; lung allergy; lung inflammation; respiratory disease; ds. AB297695/ XXX AB29 XXX AB29 XXX XXX I7-0 XXX W Huma. XXX Huma. XXX Huma. XXX antii XXY antii XXY Abmo. XXX Hung. XXX Hung. XXX Hung. XXX Hung. XXX Hung. XXX Hung. XXX Phomo. XX

Homo sapiens

WO200285308-A2

31-OCT-2002

23-APR-2002; 2002WO-US013135.

24-APR-2001; 2001US-0286137P.

(EPIG-) EPIGENESIS PHARM INC.

Katz E, Pabalan J, Aguilar D; Sandrasagra A, Ka u, Shahabuddin S; Li Y, Sar Tang L, Nyce JW, I Miller S,

WPI; 2003-229219/22.

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone

Disclosure; SEQ ID NO 12937; 872pp; English.

first activities teached to a high an interaction teached to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antisthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a treventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antialemmatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of adenosine receptor, producing bronchodilation, increasing bronchoconstriction, lung allergies, or a respiratory disease or condition, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO The invention relates to a novel pharmaceutical composition, which has at ftp.wipo.int/pub/published_pct_sequences

Sequence 20 BP; 3 A; 7 C; 5 G; 5 T; 0 U; 0 Other;

Gaps ö Length 20; Indels 52.4%; Score 11; DB 10; L 100.0%; Pred. No. 8.3e+03; iive 0; Mismatches 0; Query Match 52.4 Best Local Similarity 100. Matches 11, Conservative

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7 GAGCGGAGCAA 17 16 GAGCGGAGCAA

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ABD30726/c ID ABD30726 standard; DNA; 20 BP. RESULT 15

29-JUL-2004 (first entry) ABD30726; BXBX8X44444

Human CCR3-derived oligonucleotide SEQ ID 12937.

Human; antisense; bronchoconstriction; allergy; hyposecretion; pain; respiratory tract inflammation; adenosine sensitivity; lung; cancer; surfactant depletion; antiallergic, antiinflammatory; antiasthmatic; analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis; beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction; respiratory distresses syndrome; allergic rhinitis; pulmonary hypertension; emphysema; chronic obstructive pulmonary disease; cancer; bronchitis; pulmonary transplantation rejection; ss; primer.

sapiens. Homo WO200285309-A2

31-OCT-2002.

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This invention describes a novel composition (a) a first active agent, comprising oligonucleotides, effective for alleviating bronchoconstriction, respiratory tract inflammation, allergies and reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors, surfactant depletion or hyposecretion, when administered to a mammal. The coligonucleotides are derived from a gene encoding or regulating expression of a target polypetide associated with lung airway or lung dysfunction or cancer and can be anti-sense to the corresponding mRNA. The invention also describes a kit, that comprises: (a) a delivery device, in separate containers, (b) the oligonucleotides, (c) instructions for adding a carrier and for use of the kit. The composition of the invention has antiallergic, antiinflammatory, antiathmatic, analgesic, hypotensive, immunosuppressive and cytostatic activity, is a beta-adrenergic agonist. The composition is useful for preventing or treating a respiratory, lung or mallymant disease. The administered composition comprises oligo and is administered to reduce the production or availability, or to increase the degradation of the target mRNA or to reduce the amount of target polypeptide present in the lungs. The pulmonary obstruction, and/or bronchoconstriction are associated with a limital ammation, and/or bronchoconstriction are associated with the support of the control of the amount of the support of the control of the amount of target polypeptide present in the lungs. The control of the support of the amount of target polypeptide present in the lungs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     with a disease or condition such as pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary transplantation rejection, pulmonary infections, bronchitis or cancer. The reduced adenosine content of the anti-sense oligos corresponding to thymidines present in the target RNA serves to prevent the breakdown of the oligonucleotides into products that free adenosine into the system e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to prevent any unwanted effects due to it
                                                                                                                                                                                                                                                                                                                                          Pharmaceutical composition for treating asthma, has antisense oligonuclectide containing less percentage of adenosine, targeted to nucleic acids associated with lung airway or lung dysfunction, and
                                                                                                                                                                                                 Katz E, Pabalan J, Aguilar D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 15; SEQ ID NO 12937; 763pp; English.
                                                                                                                                                                                              Li Y, Sandrasagra A, Ka
Tang L, Shahabuddin S;
                             23-APR-2002; 2002WO-US013143.
                                                                                   24-APR-2001; 2001US-0286036P.
                                                                                                                                           (EPIG-) EPIGENESIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                bronchodilating agent
                                                                                                                                                                                                                                                                                    WPI; 2003-093058/08
                                                                                                                                                                                                    Nyce JW, 1
Miller S,
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52.4%; Score 11; DB 11; Length 20; 100.0%; Pred. No. 8.3e+03; Live 0; Mismatches 0; Indels Sequence 20 BP; 3 A; 7 C; 5 G; 5 T; 0 U; 0 Other; 11; Conservative Local Similarity Query Match Best Loca Matches

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Gaps

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Search completed: September 12, 2005, 17:04:30 Job time : 179 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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	22	12	57.1	25		US-10-956-157-278869	Sequence	278869,	
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•	APPLIC	CANT: Me	APPLICANT: Medironic, Inc	Inc.					
• •	APPLIC	ZANT:	APPLICANT: Kaemmerer, William F	Wil	liam				
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Query Match 100.0%; Score 21; DB 19; Length 21; Best Local Similarity 100.0%; Pred. No. 0.0072; Matches 21; Conservative 0; Mismatches 0; Indels

RESULT 2

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APPLICANT: Kaemmerer, william F.
TITLE OF INVENTION: Freatment of Neurodegenerative Disease Through Intracranial Delive
TITLE OF INVENTION: SIRNA
TITLE OF INVENTION: SIRNA
TITLE OF INVENTION: SIRNA
CURRENT APPLICATION NUMBER: US/10/721,693
CURRENT FILING DATE: 2003-11-25
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 21
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PRIOR APPLICATION NUMBER: 10/721,693
PRIOR FILING DATE: 2003-11-25
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 21
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GENERAL INFORMATION:
APPLICANT: Meditonic, Inc.
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                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
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US-10-721-693-2/c
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              Sequence 3, Application US/10721693
Publication No. US20040162255A1
Publication No. US20040162255A1
Publication No. US20040162255A1
APPLICANT: Nedtronic, Inc.
APPLICANT: Kaemmerer, William F.
APPLICANT: Remmerer, William F.
TITLE OF INVENTION: Tractment of Neurodegenerative Disease Through Intracranial Deliv TITLE OF INVENTION: 81RNA
FILE REPERENCE: P11089.00
CURRENT APPLICATION NUMBER: US/10/721,693
CURRENT APPLICATION NUMBER: 2003-11-25
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Medironic, Inc.
APPLICANT: Medironic, Inc.
APPLICANT: Recumerer, William F.
TITLE OF INVENTION: Treatment of Neurodegenerative Disease Through Intracranial Deliv
TITLE OF INVENTION: SIRNA
FILE REFERENCE: P11089.02
CURRENT APPLICATION NUMBER: US/10/852,997
CURRENT FILING DATE: 2004-05-25
PRIOR APPLICATION NUMBER: 10/721,693
PRIOR FILING DATE: 2003-11-25
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.1
SEQ ID NO
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                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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Pred. No. 0.0072;
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1 Similarity 100.0%; Pred. No. 0.0
21; Conservative 0; Mismatches
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US-10-652-997-3
; Sequence 3, Application US/10852997
; Publication No. US20040220132A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence I, Application US/10852997; Publication No. US20040220132A1; GENERAL INFORMATION: APPLICANT: Medironic, Inc.
                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 21; Conserva
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US-10-852-997-1
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LENGTH: 21
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GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REPERENCE: 3527.1
CURRENT APLICATION NUMBER: US/10/719,956
CURRENT FILING DATE: 2003-11-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1811, Application US/10809189; Publication No. US20050048531A1
GENERAL INFORMATION: Michael Mittmann
APPLICANT: Michael Mittmann
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.;
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 310.1
CURRENT APPLICATION NUMBER: US/10/809,189
CURRENT FILING DATE: 2004-03.25
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FSSEEE for Windows Version 4.0
SEQ ID NO 18111
                    APPLICANT: David Mack
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 310.1.1
CURRENT APPLICATION NUMBER: US/10/809,189
CURRENT PILING DATE: 2004-03.25
PRIOR PILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 127806
SEQ ID NOS: 127806
SEQ ID NO 18110
LENGTH: 25
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100.0%; Pred. No. 4.6e+02;
iive 0; Mismatches 0;
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100.0%; Pred. No. 4.6e+02;
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Best Local Similarity 100.0%; Pred. No. ...
Marches 13; Conservative 0; Mismatches
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      APPLICANT: Michael Mittmann
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Best Local Similarity 100.
Matches 13; Conservative
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CRGANISM: Mus musculus
US-10-809-189-18110
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; Sequence 4, Application US/2004022013241
; Sequence 4, Application No. US2004022013241
; GENERAL INFORMATION:
; APPLICANT: Medironic, Inc.;
; APPLICANT: Medironic, Inc.;
; APPLICANT: Assemmerer, William F.
; TILE OF INVENTION: Treatment of Neurodegenerative Disease Through Intracranial Deliv,
; TILE OF INVENTION: SiRNA
; TILE OF INVENTION: SiRNA
; TILE OF INVENTION: SiRNA
; TILE OF INVENTION: UNMBER: US/10/852,997
; CURRENT APPLICATION NUMBER: 10/721,693
; RRIOR FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 53
; SOFTWARRE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 21
                                                                                                                                                                                                                APPLICANT: Medicalia, inc.
APPLICANT: Medicalia, inc.
APPLICANT: Machine, inc.
APPLICANT: Kaemmerer, William F.
TITLE OF INVENTION: Treatment of Neurodegenerative Disease Through Intracranial Deliv
TITLE OF INVENTION: SIRM,
FILE REFERENCE: P11089.02
CURRENT APPLICATION WHEBE: US/10/852,997
CURRENT FILING DATE: 2004-05-25
PRIOR APPLICATION NUMBER: 10/721,693
PRIOR FILING DATE: 2003-11-25
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.1
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0.12;
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                                                                                                                                ; Sequence 2, Application US/10852997; Publication No. US20040220132A1; GENERAL INFORMATION: APPLICANT: Meditronic, Inc.
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CCAAGAGCGAACGAA 3
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100.0%;
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Best Local Similarity 100.
Matches 19; Conservative
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ORGANISM: Homo sapiens
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CORGANISM: Homo sapiens
US-10-852-997-4
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Best Local Similarity
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US-10-809-189-18110/c
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US-10-852-997-4/C
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LENGTH: 21
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TYPE: DNA
CORGANISM: Mus musculus
US-10-719-900-49468
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US-10-719-900-272193
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US-10-719-900-49468
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US-10-098-263B-35321/c

Sequence 35221, Application US/10098263B

Publication No. US20030104410A1

GENERAL INFORMATION:

APPLICANT: Mittman, Michael

TITLE OF INVENTION: Human Microarray

FILE REFERENCE: 31.8. Human Microarray

FILE REFERENCE: 31.8. Human Microarray

CURRENT APPLICATION NUMBER: US/10/098,263B

CURRENT APPLICATION NUMBER: 05/276,759

PRIOR PILING DATE: 2001-03-16

NUMBER OF SEQ ID NOS: 131066

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 425371, Application US/10719956;
Publication No. US20040146910A1
GENERAL INFORMATION:
APPLICAMT: Xue Mei Zhou
ITILE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REFERENCE: 3527.1
CURRENT FILING DATE: 200311-20
PRIOR PILING DATE: 20021120
PRIOR FILING DATE: 20021120
PRIOR FILING DATE: 20021120
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 425371
LENGTH: 25
                                                                                                                                                                                                        61.9%; Score 13; DB 22; Length 25; 100.0%; Pred. No. 4.6e+02; Live 0; Mismatches 0; Indels
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PRIOR APPLICATION NUMBER: 60/427,836
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 699466
SEQ TWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 201094
LENGTH: 25
                                                                                                                     TYPE: DNA
CRGANISM: Rattus norvegicus
US-10-719-956-201094
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US-10-719-956-425371
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Matches 13; Conservative
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Best Local Similarity
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CORGANISM: Homo sapien
US-10-098-263B-35321
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US-10-719-956-425371
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; Sequence 272193, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse; FILE REFERENCE: 3528.1
; CURRENT FILING DATE: 2003-11-20
; PRIOR FILING DATE: 2003-11-20
; PRIOR FILING DATE: 2002 11 20
; RIORERION DATE: 2002 11 20
; RIORERION OF SEQ ID NOS: 982914
; SEQ ID NO 272193
; LENGTH: 25
Sequence 49468, Application US/10719900
; Sequence 4966, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
    APPLICANT: Xue Mei Zhou
    TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
    FILE REFERENCE: 3528.1
; CURRENT FILING DATE: 2003-11-20
    RIOR RPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 49468
; LENGTH: 25
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Matches 12; Conservative
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Sequence 11, Appl
Sequence 202, Appl
Sequence 202, Appl
Sequence 81, Appl
Sequence 14051, A
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Sequence 42, Appl
Sequence 8, Appli
Sequence 5859, Ap
Sequence 5, Appli
Sequence 4854, Ap
Sequence 4854, Ap
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Sequence 81, Appl
Sequence 46, Appl
Sequence 3, Appli
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Sequence 18111, A
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Sequence 66427, A
Sequence 66438, A
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                                                                  September 12, 2005, 16:40:43; Search time 58 Seconds (without alignments) 592.445 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                /cgn2_6/ptodata/1/lna/5A_COMB.seq:*
/cgn2_6/ptodata/1/lna/5B_COMB.seq:*
/cgn2_6/ptodata/1/lna/6A_COMB.seq:*
/cgn2_6/ptodata/1/lna/6B_COMB.seq:*
/cgn2_6/ptodata/1/lna/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/lna/pcTUS_COMB.seq:*
        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-3196-196G-18111

US-09-172-045-31

US-09-312-25-26

US-09-312-5228-31

US-09-396-196G-14051

US-09-396-196G-14051

US-09-396-196G-18094

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US-09-396-196G-6428

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US-09-396-196G-6428

US-09-396-196G-6438

US-09-396-196G-6438

US-09-319-255-5

US-09-319-255-5

US-09-319-255-5

US-09-311-7728-4855

US-09-311-7728-4855

US-09-311-7728-4855

US-09-316-416-81

US-08-360-416-81
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US-09-422-978-10903
US-09-198-452A-5309
                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                      1202784 segs, 818138359 residues
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                                               OM nucleic - nucleic search, using sw model
                                                                                                                                  1 aaccaagagcggagcaacgaa 21
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Gapop_60.0 , Gapext 60.0
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                                                                                                          US-10-721-693-1
21
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Match Length
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                                                                                                                                                       Scoring table:
                                                                                                                                                                                                          Word size :
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19, Appl
72, Appli
2, Appli
3, Appli
63, Appli
63, Appli
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63, Appli
65, Appli
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7356, Ap
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Sequence 6
Sequence 2
Sequence 6
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Sequence 4
Sequence 7
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Sequence
Sequence
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Sequence 6
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Sequence 18111, Application US/09396196G

Patent No. 6821724

GENERAL INFORMATION:

APPLICANT: Michael Mittmann

APPLICANT: David Mack

APPLICANT: Affymetrix. Inc.

TITLE OF INVENTION: Methods of Genetic Analysis

FILE REFERENCE: 3101.1

CURRENT APPLICATION NUMBER: US/09/396,196G

CURRENT APPLICATION NUMBER: 60/100,678

PRIOR APPLICATION NUMBER: 60/100,678

PRIOR PILING DATE: 1998-09-17

NUMBER OF SEQ ID NOS: 127806

SOFTWARE: FRAESEQ for Windows Version 4.0

SEQ ID NO 18111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastESEQ for Windows Version 4.0
SEQ ID NO 18110
                                                                                                                                                                                                                                              US-09-106-075A-65
US-09-270-767-62514
US-08-379-926A-4
US-09-396-196G-7356
                              US-09-922-146-11

US-10-023-649A-19

US-09-210-896-22

US-08-210-896-22

PCT-US93-12078-2

PCT-US93-12078-3

US-08-210-762E-63

US-09-106-075A-63

US-09-106-075A-63

US-09-210-762E-65

US-08-210-762E-65
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; ORGANISM: Mus musculus
US-09-396-196G-18110
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Matches
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US-09-172-045-31
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                                                                                              Length 25;
                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Kirschner, Mark W.
APPLICANT: Kinoshita, No. 6066460iyuki
TITLE OF INVENTION: METHOD FOR CLONING SECRETED PROTEINS
TITLE FEFERENCE: HMV-022.01
CURRENT APPLICATION NUMBER: US/09/121,920
CURRENT FILING DATE: 1998-07-24
EARLIER PELLORION NUMBER: 60/053,586
EARLIER FILING DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 31, Application US/09172045
; Batent NO. 6277594
; GENERAL INCORMATION:
APPLICANT: Mikoshiba, Katsuhiko
APPLICANT: Makabi Jun
APPLICANT: Nagai, Takeharu
; APPLICANT: Nagai, Takeharu
; APPLICANT: Nakata, Katsunori
; TITLE OF INVENTION: Neurogenesis Inducing Gene
FILE REFERENCE: Hiraki-03497
; CURRENT APPLICATION NUMBER: US/09/172,045
; CURRENT FILING DATE: 1998-10-08
; EARLIER FILING DATE: 1998-03-31
; EARLIER FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 40
; NUMBER OF SEQ ID NOS: 40
; SEQ ID NO 31
LEARLIER FILING DATE: 1998-04-30
; SEQ ID NO 31
LEARLIER FILING DATE: 1006-04-30
; SEQ ID NO 31
LEARLIER FILING DATE: 1006-04-30
; SEQ ID NO 31
LEARLIER FILING DATE: 2.0
                                                                                                DB 4; Le
                                                                                  61.9%; Scor.
100.0%; Pred. No. ...
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ORGANISM: Artificial Sequence
                                                                              Query Match
Best Local Similarity 100.
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; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-18111
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Best Local Similarity
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Best Local Similarity
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; ORGANISM: primer
US-09-121-920-26
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US-09-172-045-31
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LENGTH: 20
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GENERAL INFORMATION:
APPLICANT: KIM, Jeong Joon; SJ HIGHTECH Co., Ltd.
APPLICANT: KIM, Cheol Min
APPLICANT: KIM, Cheol Min
APPLICANT: KIM, Cheol Min
FILE REPERBERCE: PPOSO2/OFCT
CURRENT APPLICATION NUMBER: US/09/980,052
CURRENT FILING DATE: 2001-11-28
FRIOR REPERIONE: PPOSO2/OFCT
CURRENT PAPLICATION NUMBER: KR 10-1999-0019631
FRIOR APPLICATION NUMBER: KR 10-1999-0019632
FRIOR APPLICATION NUMBER: KR 10-1999-0019633
FRIOR APPLICATION NUMBER: KR 10-1999-0019633
FRIOR APPLICATION NUMBER: KR 10-1999-0019635
FRIOR APPLICATION NUMBER: KR 10-1999-0019635
FRIOR APPLICATION NUMBER: KR 10-1999-0019635
FRIOR PILING DATE: 1999-05-29
FRIOR PILING DATE: 1999-05-29
FRIOR APPLICATION NUMBER: KR 10-1999-0019635
FRIOR PILING DATE: 1999-05-29
FRIOR APPLICATION NUMBER: KR 10-2000-0018189
FRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 243
SOFTWARE: KOPALENT 1.71
SEQ ID NO 202
LENGTH: 20
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-342-325C-31
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Indels
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                                                                                                                                                                                                                                                                                                                                                 APPLICANT: ATANGA, JUNIORA APPLICANT: Nagai, Takeharu
APPLICANT: Nagai, Takeharu
APPLICANT: Katsunori, Nakata
TITLE OF INVENTION: Neurogenesis Inducing Gene
FILE REFERENCE: HIRAKI-03814
CURRENT APPLICATION NUMBER: US/09/342,325C
CURRENT PILING DATE: 1999-06-30
PRIOR PILING DATE: 1998-06-30
PRIOR PILING DATE: 1998-04-31
PRIOR PILING DATE: 1998-04-30
PRIOR PILING DATE: 1998-04-30
PRIOR PILING DATE: 1998-04-30
PRIOR PILING DATE: 1998-04-30
PRIOR PILING DATE: 1998-09-28
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PATEURIN Ver. 2.0
SEQ ID NO 31
LENGTH: 20
Mismatches
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; Sequence 31, Application US/09342325C
; Patent No. 6500637
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Patent No. 6670130
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ORGANISM: Artificial Sequence
  11; Conservative
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                                 0; Indels
                                                                                                                                                                                                  RESULT 9
US-09-196-196G-18094/C
Sequence 18094, Application US/09396196G
Patent No. 6821224
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: APPLICANT: AFFWERTIX, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT FILING DATE: 1999-09-15
PRIOR PILICATION NUMBER: 06/100,678
PRIOR FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
US-09-396-196G-18109/C
; Sequence 18109, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
         Pred. No. 2e+03;
                                    0; Mismatches
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CURRENT FILING DATE: 1999-09-15
PRIOR PILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18109
LENGTH: 25
   100.08;
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Best Local Similarity 100.
Matches 11; Conservative
                                    11; Conservative
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Matches 11; Conservative
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                                                                                                                               7 CCAAGAGCGGA 17
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US-09-396-196G-18094
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Best Local Similarity
Matches 11; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTIONS AND METHODS FOR ANALYSIS OF LIPID METABOLISM AND FILE OF INVENTION: ANIMAL MODELS AND METHODS FOR ANALYSIS OF LIPID METAFILE OF INVENTION: OF PHARMACEUTICAL AND PESTICIDAL AGENTS THAT MODULATE LIPID METAFILE REPERENCE: 7326-101, EX99-004

CURRENT APPLICATION NUMBER: 1899-06-14

NUMBER OF SEQ ID NOS: 95

SOFTWARE: PATENTIN VERSION 3.1

LENGTH: 22
                                                                                     ; OTHER INFORMATION: sequence of probe or primer for detecting Mycobacterium porcinum US-09-980-052-202
                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52.4%; Score 11; DB 4; Length 25;
                                                                                                                                                                          52.4%; Score 11; DB 4; Length 20;
100.0%; Pred. No. 2e+03;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 8

US-09-396-196G-14051
; Sequence 14051, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
    APPLICANT: Mitcheal Mittmann
; APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: AFFWERTIX, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: 60/100,678
FRIOR PILING DATE: 1999-09-15
; WINGRENT FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: ReatSEQ for Windows Version 4.0
; SEQ ID NO 14051
; TUNDE OF SET SECT OF SECTION SEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 81, Application US/09332522E
; Patent No. 6781028
; GENERAL INFORMATION:
; APPLICANT: Costa, M.
; APPLICANT: Bloon, S.
; APPLICANT: Bloon, S.
; APPLICANT: Homberger, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Oligonucleotide US-09-332-522E-81
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                   11; Conservative
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Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                                                                                                                     Best Local Similarity
Matches 11; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 7
US-09-332-522E-81/c
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Gaps
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Patent No. 5834183
GENERAL INFORMATION:
APPLICANT: Ranum, Laura P.W.
APPLICANT: Chung, Ming-Yi
APPLICANT: Zoghbi, Huda Yi
TILLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
Patent No. 5834183
TITLE OF SEQUENCES: 85
NUMBER OF SEQUENCES: 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS: AS ADDRESSE: Mueting, Raasch, Gebhardt & Schwappach, P.A. STREET: P.O. Box 581415
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    52.4%; Score 11; DB 4; Length 25; 100.0%; Pred. No. 2e+03; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION UNMER:
FILING DATE: 28-JUN-1994
CLASSIFICATION: 435
ATTONREY/AGERT INFORMATION:
NAME: MCCOrmack, Myra H.
REGISTRATION NUMBER: 36,602
REFERENCE/POCKET UNMER: 110.00030120
TELECOMMULCATION:
TELEPHONE: 612-305-1217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 52.4%; Score 11; DB 2; Best Local Similarity 100.0%; Pred. No. 2e+03; Matches 11; Conservative 0; Mismatches C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Pred. No. 2e+
:ive 0; Mismatches
                                                                 CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 66438
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 55458-1415
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 52.4
Best Local Similarity 100.
Matches 11; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 GAGCGGAGCAA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 GAGCGGAGCAA 20
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                                                                                                                                                                                                                                                                                                                            TYPE: DNA
CORGANISM: mus musculus
US-09-396-196G-66438
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US-08-267-803B-81
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"and. No. 28+03;
0; Indels
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US-09-396-196G-66426

; Sequence 66426, Application US/09396196G
; Patent No. 6621724
; GENERAL INFORMATION:
; APPLICANT: Michael Mitchael Mitchael Mitchael Mitchael Mitchael Mitchael Machael David Mack
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REPERBNCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FBSEQ for Windows Version 4.0
; SEQ ID NO 66426
; LENGTH: 25
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| Sequence 6427, Application US/09396196G |
| Patent No. 6821724 |
| GENERAL INFORMATION: |
| APPLICANT: Michael Mittmann |
| APPLICANT: David Mack |
| APPLICANT: David Lockhart |
| APPLICANT: David Lockhart |
| APPLICANT: Affymetrix, Inc. |
| TITLE OF INVENTION: Methods of Genetic Analysis |
| FILE REPERBNCE: 3101.1 |
| CURRENT APPLICATION NUMBER: US/09/396,196G |
| CURRENT FILING DATE: 1999-09-15 |
| PRIOR PILING DATE: 1998-09-17 |
| NUMBER OF SEQ ID NOS: 127806 |
| SEQ ID NO 66427 |
| LENGTH: 25 |
| LENGTH: 2
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APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: AFF/metrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52.4%; Scor.
100.0%; Pred. No. co.
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; Sequence 66438, Application US/09396196G
; Patent No. 6821724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 11; Conservative
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; ORGANISM: mus musculus
US-09-396-196G-66427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) ORGANISM: mus musculus
US-09-396-196G-66426
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Best Local Similarity
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US-09-396-196G-66427
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Matches

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RESULT 15
US-08-848-810-42

i Sequence 4.2, Application US/08848810

patent No. 6074851

GENERAL INFORMATION:

APPLICANT: Deibel Jr., M. R.

APPLICANT: Wilson, C. L.

ITLE OF INVENTION: Catalytic Macro Molecules Having DCD25B

TITLE OF INVENTION: Like Activity

NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:

ADDRESSE: Pharmacia & Upjohn Company

STREET: 301 Henrietta Street

CITY: Kalamazoo

STATE: MI

COUNTRY: USA

ZIP: 49001

COMPUTER: IBM PC Compatible

OPERATION SYSTEM: PetentIn Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/08/88.810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WOOCLCO, Thomas A.
REGISTRATION NUMBER: 35,004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 616-833-7914
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: MUCLEIC acid
STRANDEDNESS: single
TYPE: MUCLEIC acid
STRANDEDNESS: single
19 AACCAAGAGCG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) MOLECULE TYPE: CDNA

) HYPOTHETICAL: NO

) ANTI-SENSE: NO

US-08-848-810-42
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0; Gaps
Score 11; DB 3; Length 30; Pred. No. 2e+03; 0; Mismatches 0; Indels
Query Match 52.4
Best Local Similarity 100.
Matches 11; Conservative
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7 GAGCGGAGCAA 17 GAGCGGAGCAA 14 Search completed: September 12, 2005, 18:11:00 Job time : 60 secs

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1M0324C10 1M0341F08

AU256438 5009-0-54

5009-0-55

2M0164A07

5009-0-18 5009-0-58 5009-0-59

ABF--06-D

1M0281114

2M0096015

5009-0-40

5009-0-8

M0049D09 .M0202J03

score:

Title: Perfect

Sequence:

OM nucleic

Run on:

Scoring table:

Word size :

Searched:

Database :

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1. .25
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/tismue_type="leaf"
/dev stage="leaf"
/dev stage="adult"
/lab_host="DH109"
/clone_lbb="ll19 - RescueMu Grid AA"
/clone_lbb="ll19 - RescueMu Grid AA"
/noce="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHi; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.radb.iastate.edu' and follow the links for
'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA
was extracted from leaf strips, double digested using
                                                                                                                                                                                                                                                                                                                                                          25 bp DNA linear GSS 20-OCT-2003
- RescueMu Grid AA Zea mays genomic, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Bermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.
(bases 1 to 25)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 650 723 2227
Fax: 650 723 2227
Fax: 650 725 8221
Foreit is albotosterior of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1119027 row: E column: 01
Class: transposon-tagged.
Location/Qualifiers
BM398612
AZ23642
AZ423444
AZ823837
BM398108
BM398108
BM398156
BM400852
AZ853454
AZ853454
AZ8531954
BM399525
BM399525
AZ461197
AZ461197
AZ562375
AZ65121
AZ562375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                               BM398108
BM398156
BM400852
AZS93454
AZ822792
BM396198
                                                                                                                                       BM399525
BM399548
CF311108
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AZ491197
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BM399155
                          4Z326642
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580.290 Million cell updates/sec
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                                                                                       September 12, 2005, 15:58:45; Search time 1377.5 Seconds
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AZ593480 IM041
BM399181 G099-
BM399181 G099-
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AG203460 Pan C
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AG190199 E
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              GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                             34239544 seqs, 19032134700 residues
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                                                               - nucleic search, using sw model
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AJ593450
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Gapop_60.0 , Gapext 60.0
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995-est3:

995-est43:

995-est43:

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995-9881:

995-9881:
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Match Length
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Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC); 52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea (E-mail:redstone@mail.kribb.re.kr, URL:http://phs.grc.kribb.re.kr/, Tel:82-42-866-7181, Fax:82-42-866-4409) Clones are derived from the chimpanzee BAC library RP-43 This BAC end was generated during the R&D process and may have higher chance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AZ599480 19 bp DNA linear GSS 13-DEC-2000 1M0414C20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0414C20 R, genomic survey sequence.
                                                                                                                                                                                                      AG201067 30 bp DNA linear GSS 06-MAR-2004
Pan troglodytes DNA, clone: RP43-083G08.TJ, genomic survey
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Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J., Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H. BAC end sequences of Library RP-43 Unpublished
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/clone_lib="RP-43 Chimpanzee Male BAC Library"
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100.0%; Pred. No. 1.6e+05;
tive 0; Mismatches 0;
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/organism="Pan troglodytes"
  Mismatches
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/db_xref="taxon:9598"
/clone="RP43-083G08.TJ"
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R.Site 2 : Porre
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LIBRARY
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                                             8 AGCGGAGCAA 17
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Concact: Wilson RK
Washington University School of Medicine
4444 Forest Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, Linin
This clone is available royalty-free through LiNi, contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
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                                                                                                                                                                                                                                                                                                                                                                      EST 24-MAY-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Materston,R., Williamson,A., Wohldmann,P. and
BamHI and BglII, and ligated to form circular plasmids.
DH10B cells were transformed and then screened on LB
plates with ampicillin."
                                                                                                                                                                                                                                                                                                                                                               R60473
yhl3g06.rl Soares infant brain 1NIB Homo sapiens cDNA clone
IMAGE:43057 5' similar to SP:SYNP_RAT P22831 ;, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Possible reversed clone: similarity on wrong strand Seg primer: M13Rpl High quality sequence stop: 1. Location/Qualifiers
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                                                                                                           Score 10; DB 9; Length 25;
Pred. No. 1.6e+05;
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                                                                                             47.6%; Scor.
100.0%; Pred. No. ...
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/db_xref="GDB:415598"
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/clone="IMAGE:43057"
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VERSION KEYWORDS SOURCE ORGANISM

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/clone_lib="Moouse 10kb plasmid UUGCIM library"
/clone_lib="Woouse 10kb plasmid UUGCIM library"
/note="Westor: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources
/nttp://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt enda-repaired with T4 DNA polymerase and T4
polynuclectide kinase. Adaptor oligonuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil | 4732114 | gb | AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

(bases 1 to 19)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Menen, B., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Miderhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
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Arabidopsis thaliana T-DNA flanking sequence, left border, clone 380F06, genomic survey sequence.
                                                                                                                                                                                                                                                                                           E., SLC,
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                                                                                                                                                                                         Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030
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SSS; left border: T-DNA flanking sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                             Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@qenetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0414 row: C column: 20
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone="UUGC1M0414C20"
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As Submitted (12-020)

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                                                                                                                             Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Caboche, M. and Lecharny, A.
T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST from Tetrahymena thermophila, strain CU428.1, growing cells Unpublished (2002)
Contact: Turkwhitz AP
Molecular Genetics and Cell Biology
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Hymenostomatida; Tetrahymenina; Tetrahymena.
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Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
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920 E. 58th Street, Chicago, IL 60637, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Arabidopsis thaliana"

    .20
    /note="T-DNA flanking sequence"

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/cultivar="Wassillewskija"
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Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
                                                                                                                                                                                                                                                                                                                                                                                              EMBO Rep. 3 (12), 1152-1157 (2002)
22363535
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Best Local Similarity 100.
Matches 9; Conservative
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Tel: 801 585 5606
Fax: 801 585 7177
                    26 AACCAAGAG 18
                                                                                                                                                                                                                                                                                Mus musculus
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KEYWORDS
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ORGANISM
                                                                                                                                                DEFINITION
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AZ861916
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Clones are derived from the chimpanzee BAC library RP-43 This BAC end was generated during the R&D process and may have higher chance
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSS 06-MAR-2004
                                                                                  /mol_type="mRNA"
| Strain="CTG1481."
| db xref="taxon:591"
| clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
| /note="Vector: BlueScriptz SKt, betails on library
| preparation can be found in Chilcoat and Turkewitz (2001)
| Proc. Natl. Acad. Sci USA, 98: 8709-8713."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J., Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H. BAC end sequences of Library RP-43 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AG203460 28 bp DNA linear GSS 06 Pan troglodytes DNA, clone: RP43-087P23.TJ, genomic survey
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/clone_lib="RP-43 Chimpanzee Male BAC Library"
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    .25
    /organism="Tetrahymena thermophila"

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42.9%; Score 9; DB 4; Ler
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches 9; Conservative 0; Mismatches 0;
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    .28
    /organism="Pan troglodytes"

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/db_xref="taxon:9598"
/clone="RP43-087P23.TJ"
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                    Location/Qualifiers
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R.Site 1 : EcoRI
R.Site 2 : EcoRI.
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Seq primer: T3
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Gaps

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Conservative

1 AACCAAGAG

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymorase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gilfa732114 [gp] [AR129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
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           GSS 21-FEB-2001
                                                                                                                                                                                                                                                                                           Bukaryotta, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 30)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longarter, S., Mahmoud, M., Meeneh, E., Pedersen, T., Reilly, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Diame, Wolle genome scaffolding with paired end reads from 10kb Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
A2861916 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0168K17R Muse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0168K17 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clome_lib="Mouse lokb plasmid UUGCNM library."
/note="Vector: PWD4Znv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Insert Length: 10000 Std Error: (
Plate: 0.168 row: K column: 17
Seq primer: CACAGGAAACAGCTATGACC
Class: plasmid ends
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/strain="C57BL/6J"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="UUGC2M0168K17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: ddunn@genetics.utah.edu
                                                                                                                                                                                                                           Mus musculus (house mouse)
                                                                                                                                                          AZ861916.1 GI:13058714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="Male"
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RESULT 9 AJ598448/c DEFINITION

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ORGANISM

SOURCE

REFERENCE AUTHORS

ACCESSION VERSION KEYWORDS REFERENCE AUTHORS TITLE JOURNAL

COMMENT

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TITLE

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Eukaryota; Alvelata; Ciliophora; Oligohymenophorea;
Eukaryota; Alvelata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymenia.

E Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E., Frankel, J. and Klobutcher, L.
Frankel, J. and Klobutcher, L.
Confact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 4374
Email: apturkew@midway.uchicago.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 bp mRNA linear EST 25-AFR-2002
AU256829 3'-directed mouse cDNA library Mus musculus cDNA clone
AU256829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/strain="CU428.1"
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/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/clone_lib="Vector: BlueScript2 SK+; Details on library
preparation.can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Kato, K. and Matoba, R.
Generation of expressed sequence tags from mouse brain Unpublished (2002)
Contact: Kikuya Kato
Graduate School of Biological Sciences
Nara Institute of Science and Technology
8916-5 Takayama, Ikoma, Nara 630-0101, Japan
Tel: 81-743-72-5581
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/mol_type="mRNA"
/db_xref="taxon:10090"
/db_cref="taxon:10090"
/tissue type="brain"
/clone_lib="3'-directed mouse cDNA library"
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URL:http://love2.aist-nara.ac.jp/BED/index.html.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Tetrahymena thermophila"
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        Tetrahymena thermophila
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AU256829/c
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FOR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versaillee). The DNA fragment(s) resulting from the PCR ware directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbagap.versailles.inra.fr/publiclines/. This sequence has program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.info.piogen.fr).

Location/Qualifiers
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Etrahymena thermophila cDNA, mRNA sequence.
BM398577
                                                                                                                                                        AJ598448 15-JAN-2004 Arabidopsis thaliana T-DNA flanking sequence, right border, clone
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T-DNA integration into the Arabidopsis genome depends on sequences
                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Gore eudicots; Core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
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GSS; right border; T-DNA flanking sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="T-DNA flanking sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic_DNA"
/cultivar="Wassillewskija"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of pre-insertion sites
EMBO Rep. 3 (12), 1152-1157 (2002)
22363535
                                                                                                                                                                                                        468F11, genomic survey sequence.
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EST.
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Balzergue, S.
Direct Submission
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Best Local Similarity 100.
Matches 8; Conservative
1 AACCAAGA 8
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ORIGIN

FEATURES

DEFINITION

RESULT 10 BM398577

ઠે 용 ACCESSION VERSION KEYWORDS SOURCE

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EST 17-JAN-2002
                                                                                                                                                        /organism="Tetrahymena thermophila"
/mol type="mRNA"
/mol type="mRNA"
/doctain="CU0480.1"
/db xref="texon:591"
/clone_lib="Chilocoat/Turkewitz CDNA (large fraction)"
/note="Vector: BluesGriptz SK+; Details on library
/note="vector: BluesGriptz SK+; Details on library
/note=aration can be found in Chilocoat and Turkewitz (2001)
/proc. Natl. Acad. Sci USA, 98: 8709-8713."
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/clone lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: BluesCript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
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Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
1 (Dases 1 to 20)
Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
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5009-0-51-B10.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Tetrahymena thermophila"
920 E. 58th Street, Chicago, IL 60637, USA Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
Location/Qualifiers
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920 E. Sath Street, Chicago, IL 60637, USA
TEL: 773 702 4374
Fax: 773 702 3172
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Molecular Genetics and Cell Biology
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Location/Qualifiers
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/strain="CU428.1"
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preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
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Tetrahymena thermophila
Bukaryota, Alveolata, Ciliophora, Oligohymenophorea,
Bukaryota, Alveolata, Ciliophora, Oligohymenophorea,
Hymenostomatida, Tetrahymenina, Tetrahymenidae, Tetrahymena.

1 (bases 1 to 20)
Turkenitz, A. P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E.,
Frankel, J. and Klobutcher, L.
BST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymenina; Tetrahymenina; Tetrahymenina; Tetrahymenia; Tetrahymena.

1 (bases 1 to 20)
1 urkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E., Frankel, J. and Klobutcher, L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells Unpublished (2002)
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                                                                                                                                                                                                                                    5009-0-34-G11.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
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38.1%; Score 8; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6e+06;
Matches 8; Conservative 0; Mismatches 0; Indels
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Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
                                                                                                                                                                                                                mRNA
    0; Mismatches
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Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
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    Conservative
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BM398968 20 bp mRNA linear EST 17-JAN-2002 5009-0-51-C03.t.1 Chilcoat/Turkewitz cDNA (large fraction) Tetrahymena thermophila cDNA, mRNA sequence. BM398968.1 GI:18199021
                                                                                                                                                                    "SM Tetrahymena thermophila

SM Tetrahymena thermophila

Bukaryota; Alveolata; Ciliophora; Oligohymenophorea;

Hymenostonatida; Tetrahymenina; Tetrahymena.

Hymenostonatida; Tetrahymenina; Tetrahymena.

El (bases 1 to 20)

Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E., Frankel,J. and Klobuccher,L.

EST from Tetrahymena thermophila, strain CU428.1, growing cells

Unpublished (2002)

Contact: Turkewitz AP

Molecular Genetics and Cell Biology

University of Chicago

920 E. 58th Street, Chicago, IL 60637, USA

Tel: 773 702 3172

Fax: 773 702 3172

Email: apturkew@midway.uchicago.edu

Seq primer: T3.
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/clone lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Yector: BluesCriptz SK+, Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
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Query Match 38.1%; Score 8; DB 4; Length 20; Best Local Similarity 100.0%; Pred. No. 2.6e+06; Matches 8; Conservative 0; Mismatches 0; Indels

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: WO 2004047872-A 2 10-JUN-2004;
Medtronic, Inc. (US)
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Sequence 2 from Patent W02004047872.
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CQ824575.1 GI:49021594
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Sequence 4 from Patent W02004047872.
CQ824577.1 GI:49021598
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AX445982
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                  GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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PAT 08-OCT-2004

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Subtil, A., Parsot, C. and Dautry-Varsat, A.
Secreted chlamydia polypeptides and method for identifying such polypeptides by their secretion by a type III secretion pathway of a gram-negative bacteria
Patent: WO 0248185-A 13 20-UNA-2002;
INSTITUT PASTEUR (FR); CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CMS) (FR); INSERM (E.P.S.T.) (FR)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unclassified.

1 (Dases 1 to 22)

1 (Dases 1 to 22)

1 (Dases 2 to 22)

1 (Dases 2 to 22)

2 (Deta,M.R., Doberstein,S.K., Elson,S.L., Ferguson,K.C. and Homburger,S.A.

Animal models and methods for analysis of lipid metabolism and screening of pharmaceutical and pesticidal agents that modulate lipid metabolism.

2 (Detaion)/Qualifiers
                                                                                                                                                     DB 6; Length 21; 2.7;
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/noTe="primer"
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synthetic construct
other sequences; artificial sequences.
                                                                                                                                                   Query Match 90.5%; Score 19; DB Best Local Similarity 100.0%; Pred. No. 2.7 Matches 19; Conservative 0; Mismatches
                                                                         /mol_type="unassigned DNA" /db_xref="taxon:9606"
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Sequence 81 from patent US 6781028.
AR568156 GI:53986443
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Sequence 13 from Patent WO0248185.
AX463675
                                     1. .21
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="unknown"
/mol_type="genomic DNA"
 Medtronic, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                 3 TTCGTTGCTCCGCTCTTGG 21
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                       Treatment of neurodegenerative disease through intracranial delivery of sirna Patent: WO 2004047872-A 4 10-JUN-2004; Medtronic, Inc. (US)
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Treatment of neurodegenerative disease through intracranial delivery of sirna
Patent: WO 2004047872-A 1 10-JUN-2004;
Medironic, Inc. (US)
Location/Qualifiers
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Sequence 1 from Patent WO2004047872.
CQ824574
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Sequence 3 from Patent WO2004047872.
CQ824576
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Homo sapiens
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Matches 19; Conservative
                                                         Kaemmerer, W.F.
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CQ824574/c
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PAT 20-FEB-2004
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1 (Dases 1 to 20)

Kim,C.M., Park,H.K. and Jang,H.J.
Oligonuclectide for detection and identification of Mycobacteria Patent: US 6670130-A 202 30-DEC-2003;
Location/Qualifiers
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1 (bases 1 to 30)
Deibel,M.R. Jr., Yem,A.W. and Wolfe,C.L.
Deitalytic macro molecules having cdc25B like activity
Patent: US 6074851-A 42 13-JUN-2000;
Location/Qualifiers
                                                                                                                     Length 20;
                                                                                                                                                                                                                                                                                    linear
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                                                                                                                   Query Match 52.4%; Score 11; DB 6; Length 20; Best Local Similarity 100.0%; Pred. No. 1.1e+05; Matches 11; Conservative 0; Mismatches 0; Indels
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                31-DEC-2002;
                                                                                                                                                                                                                                                                                  AR442594 20 from patent US 6670130.
Sequence 202 from patent US 6670130.
AR442594.1 GI:42669851
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AR098219
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    /organism="unknown"
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Neurogenesis inducing genes
Patent: US 6500637-A 31 31-DE
Location/Qualifiers
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C12N15/09, A61K35/74, A61K35/76, A61K38/00, A61K48/00, PC
C07K14/47,
PC C12N1/21, C12N5/10, C12P21/02//(C12N1:91), (C12N1')
PC C12N1/21, C12N5/10, C12P21/02, C12R1:91), (C12N1')
PC C12N5/10, C12R1:91), (C12N5/10, (C12N1:91), (C12N1:91), (C12N1:91)
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Unclassified.
1 (bases 1 to 20)
Mikoshiba,K., Aruga,J., Nagai,T. and Nakata,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism='Unidentified'
Location/Qualifiers
                             57.1%; Score 12; DB 6; Lv
100.0%; Pred. No. 2.8e+04;
iive 0; Mismatches 0;
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AR268863

    .20
    /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

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JP 1999341985-A/28.
unidentified
                             Query Match
Best Local Similarity 100.
Matches 12; Conservative
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PAT 07-JUN-2002
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                                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                          Telerman, A., Amson, R. and Tuijnder, M.
Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments
Patent: WO 3032217A 1833 27-MAR-2003;
Molecular Engines Laboratories (FR)
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Muteins of interleukin-13 (il-13)
Patent: WO 0162933-A 5 30-AUG-2001;
Royal Brompton and Harefield NHS Trust (GB)
Location/Qualifiers
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                                                                                             AX736243 17 bp DNA Sequence 1833 from Patent WO03025177.
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synthetic construct
other sequences; artificial sequences.
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/db_xref="taxon:9606"
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Sequence 5 from Patent W00162933.
AX229718
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                                                                                                                                                                               Homo sapiens (human)
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PN JP 2002515742-A/27
PD 28-MAY-2002
PF 02-MAY-1997 JP 1997538892
PF 02-MAY-1996 US 60/016748,07-MAY-1996 US 60/017323 P
MARTIN R DEIBEL JR, ANTHONY W YEM, CINNY L WILSON PC
C12N15/55,C12N15/54,C12N15/62,C12N9/16,C12N9/10,C12N1/21// PC
CC Strandedness: Single;
CC Topology: Linear;
CC Topology: Linear;
CC Topology: Linear;
CC Catalytic polymer having CDC25B like activity FH Key
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Song, A.M., Chen, Y.-F. and Krensky, A.M.
RFLAT-1: a transcription factor that activates RANTES gene
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1 Similarity 100.0%; Pred. No. 1.1e+05;
11; Conservative 0; Mismatches 0; Indels
                                                      30 bp DNA lin
Catalytic polymer having CDC25B like activity.
BD195066
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unidentified
unclassified.

Jr (bases 1 to 30)
Jr. N.R.D., Yem,A.W. and Wilson,C.L.
Catalytic polymer having CDC25B like activity
Patent: JP 2002515742-A 27 28-MAY-2002;
PHARMACIA & UDJOHN CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism='Unidentified'
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Location/Qualifiers
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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JP 2002515742-A/27.
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DEFINITION Sequence 355 from Patent W00196612.
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AX402871.1 GI:21387862
KEYWORDS
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ORGANISM
Penicillium melinii
ORGANISM
Penicillium melinii
Eukaryota; Fungi, Ascomycota; Pezizomycotina; Burotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.

AUTHORS
HUMUSIANIA.
AUTHORS
HUMUSIANIA.
OUNTED STATES ENVIRONMENTAL PROTECTION AGENCY (US)
FEATURES

Location/Qualifiers
JOURNAL
ONITED STATES ENVIRONMENTAL PROTECTION AGENCY (US)

Location/Qualifiers
JOURNAL
AT.08; Score 10; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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